

##residues 1-455 ##label SCH
 REFERENCE ##cross-references GB:M33294; NID:g339744; PIDN:AAA03210.1; PID:g339745
 #journal A36555
 #authors Himmeler, A.; Maurer-Pogoy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.; Stratzmaier, C.; Adolf, G.R.
 #title DNA Cell Biol. (1990) 9:705-715
 #cross-references MUID:91090841
 #accession A36555
 #molecule-type mRNA
 #residues 1-455 ##label HIM
 #cross-references GB:M63121; NID:g339755; PIDN:AAA6754.1; PID:g339756
 #accession C36555
 #molecule-type protein
 #residues 30-38;41-53,'X',55-79,'XX',82-94,'NK','XX',100-104;
 #note the purified protein, called tumor necrosis factor binding protein, is a soluble derivative of the receptor

REFERENCE A38281
 #authors Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
 #journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:7380-7384
 #title Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of recombinant soluble TNF-binding protein.
 #cross-references MUID:91017509
 #accession A38281
 #molecule-type mRNA
 #residues 1-455 ##label GRA
 #cross-references GB:M37764
 #note the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372 as Leu, and GAC for residue 427 as Asn

REFERENCE S12057
 #authors Nophr, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann, H.; Wallach, D.
 #journal EMBO J. (1990) 9:3269-3278
 #title Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type I TNF-R, cloned using amino acid sequence data of its soluble form, encodes both the cell surface and a soluble form of the receptor.
 #cross-references MUID:91006021
 #accession S12057
 #molecule-type mRNA
 #residues 1-455 ##label NOP
 #cross-references EMBL:X55313; NID:g37223; PIDN:CAA39021.1; PID:g37224
 #note parts of soluble TNF binding protein 1, including its amino and carboxyl ends, were confirmed by protein sequencing

REFERENCE J70758
 #authors Kemper, O.; Wallach, D.
 #journal Gene (1993) 134:209-216
 #title Cloning and partial characterization of the promoter for the human p55 tumor necrosis factor (TNF) receptor.
 #cross-references MUID:94085779
 #accession J70758
 #molecule-type DNA
 #residues 1-13 ##label KEM
 REFERENCE A60231
 #authors Secklinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
 #journal Eur. J. Immunol. (1990) 20:1167-1174
 #title Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence and evidence for anti-inflammatory and immunomodulatory activities.
 #cross-references MUID:90292116
 #accession A60231
 #molecule-type protein
 #residues 41-43,'X',45-53,'X',55-57 ##label SEL
 A38258

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##authors Gatnaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Luccl III, J.A.; Jeffes, E.W.B.; Lantz, R.; Tomich, J.; Yamamoto, R.S.; Gaenger, G.A.
 #journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8781-8784
 #title Purification and characterization of an inhibitor (soluble tumor necrosis factor receptor) for tumor necrosis factor and lymphotoxin obtained from the serum ultrafiltrates of human cancer patients.
 #cross-references MUID:91062364
 #accession A38258
 #molecule-type protein
 #residues 41-60 ##label GAT
 #experimental-source cancer patient serum

REFERENCE A60594
 #authors Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.
 #journal Eur. J. Haematol. (1989) 42:270-275
 #title Isolation and characterization of a tumor necrosis factor binding protein from urine.
 #cross-references MUID:89171156
 #accession A60594
 #molecule-type protein
 #residues 41-43,'X',45-53,'V',55-57,'XK',60 ##label OLS
 #experimental-source renal failure patient urine

REFERENCE A35010
 #authors Engelmann, H.; Novick, D.; Wallach, D.
 #journal J. Biol. Chem. (1990) 265:1531-1536
 #title Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.
 #cross-references MUID:90110215
 #accession A35010
 #molecule-type protein
 #residues 41-45 ##label ENG
 #experimental-source normal urine

REFERENCE JC2404
 #authors Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.; Biosci. Biotechnol. Biochem. (1994) 58:2266-2268
 #journal Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified from human urine.
 #cross-references MUID:95128033
 #accession JC2404
 #molecule-type protein
 #residues 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201 ##label KAJ

##experimental-source urine
 COMMENT This protein is one of two known receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
 GENETICS
 #gene GDB:TNFR1
 #cross-references GDB:125913; OMIM:191190
 #map-position 12p13.2-12p13.2
 #introns 13/3; 65/1; 108/1; 158/2; 209/1; 247/1; 256/3; 353/1
 CLASSIFICATION
 #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology
 duplication; glycoprotein; receptor; transmembrane protein

KEYWORDS
 FEATURE
 1-21
 22-455
 30-211
 41-201
 44-82
 87-116
 127-167
 168-196
 212-234
 235-455
 54,145,151

SUMMARY
 #length 455 #molecular-weight 50494 #checksum 153

S. Parkhill coll. 1992-1994

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Query Match 100.0%; Score 202; DB 1; Length 455;
 Best Local Similarity 96.4%; Pred. No. 6,356-36;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 30 LVPISGDRKRDSCPOGKYHPQNSI 57
 1 lvphtgdrkrdscvcpqkyhnpqnsi 28

RESULT 2
 ENTRY 157826 #type complete
 TITLE tumor necrosis factor receptor - mouse
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999

ACCESSIONS 157826
 REFERENCE 157826
 #authors Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.
 #journal Mol. Immunol. (1993) 30:165-176
 #title Genomic organization and promoter function of the murine tumor necrosis factor receptor beta gene.

*cross-references MUID:9156721
 #accession 157826
 #status preliminary: translated from GB/EMBL/DBJ
 #molecule_type DNA
 #residues 1-454 #label RES
 ##cross-references GB:M656; NID:9202100; PIDN:AAA40465.1; PID:9202102

GENETICS
 #gene TNFR-2
 #introns 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
 CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology cytochrome receptor

KEYWORDS
 FEATURE 44-82
 SUMMARY #domain NGF receptor repeat homology #label NGF
 #length 454 #molecular_weight 50030 #checksum 4267

Query Match 83.7%; Score 169; DB 2; Length 454;
 Best Local Similarity 78.6%; Pred. No. 1,196-26;
 Matches 22; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

DB 30 LVPISGDRKRDSCPOGKYVHSKNSI 57
 1 lvphtgdrkrdscvcpqkyhnpqnsi 28

RESULT 3
 ENTRY GOMST1 #type complete
 TITLE tumor necrosis factor receptor 1 precursor - mouse
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Jun-1999

ACCESSIONS A38634; B40254; S16677; S19021; I54532
 REFERENCE A38634
 #authors Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.
 #journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834
 #title Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.

*cross-references MUID:91187865
 #accession A38634
 #molecule_type mRNA
 #residues 1-454 #label LEW
 ##cross-references GB:M60468; NID:919825; PIDN:AAA39751.1; PID:919826

REFERENCE A40254
 #authors Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, M.O.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.
 #journal Mol. Cell. Biol. (1991) 11:3020-3026
 #title Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor.

*cross-references MUID:91246168
 #accession B40254
 #molecule_type mRNA
 #residues 1-454 #label GO2
 ##cross-references GB:M60468; NID:919825; PIDN:AAA39751.1; PID:919826

REFERENCE S16677
 #authors Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissmerghs, A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J.
 #journal Eur. J. Immunol. (1991) 21:1649-1656
 #title Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis factor receptor.

*cross-references MUID:91285014
 #accession S16677
 #molecule_type mRNA
 #residues 1-454 #label BAR
 ##cross-references EMBL:X59238; NID:953578; PIDN:CAA1922.1; PID:953579

REFERENCE S19021
 #authors Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
 #journal Immunogenetics (1991) 34:338-340
 #title Molecular cloning and expression of the mouse Tnf receptor type b.

*cross-references MUID:92039815
 #accession S19021
 #molecule_type mRNA
 #residues 1-454 #label ROT
 ##cross-references EMBL:X57796; NID:954848; PIDN:CAA40936.1; PID:954849

REFERENCE I54532
 #authors Bebo, B.F.
 #journal Immunogenetics (1994) 39:450-451
 #title Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell line.

*cross-references MUID:94245292
 #accession I54532
 #status translated from GB/EMBL/DBJ
 #molecule_type mRNA
 #residues 1-454 #label RES
 ##cross-references GB:I26349; NID:9430732; PIDN:AAA59361.1; PID:9430733

COMMENT This protein is one of two distantly related receptors for both TNF-alpha (cachectin) and TNF-beta (lymphokine).

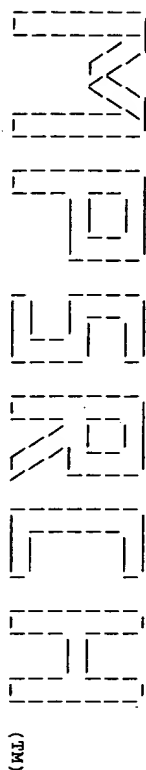
CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology duplication; glycoprotein; receptor; transmembrane protein

KEYWORDS
 FEATURE 1-29
 SUMMARY 30-454
 #domain signal sequence #status predicted #label SIG
 #product tumor necrosis factor receptor type 1 #status predicted #label MAT
 #domain extracellular #status predicted #label EXT
 30-212 #domain NGF receptor repeat homology #label NG1
 44-82 #domain NGF receptor repeat homology #label NG1
 84-126 #domain NGF receptor repeat homology #label NG2
 127-167 #domain NGF receptor repeat homology #label NG3
 168-204 #domain NGF receptor repeat homology #label NG4
 213-235 #domain transmembrane #status predicted #label MEM
 236-454 #domain intracellular #status predicted #label INT
 54,151,202 #binding site carbohydrate (asn) (covalent) #status predicted

Query Match 83.7%; Score 169; DB 1; Length 454;
 Best Local Similarity 78.6%; Pred. No. 1,196-26;
 Matches 22; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

DB 30 LVPISGDRKRDSCPOGKYVHSKNSI 57
 1 lvphtgdrkrdscvcpqkyhnpqnsi 28

RESULT 4
 ENTRY GOMT1 #type complete
 TITLE tumor necrosis factor receptor 1 precursor - rat
 ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
 DATE 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999


 (TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
 Run on: Tue Apr 18 11:05:55 2000; Maspar time 47.51 Seconds
 Tabular output not generated. 27,800 Million cell updates/sec

Title: >PEP1.PEP
 Description: (1.28) from new.pep
 Perfect Score: 202
 Sequence: 1 lvpnlgtrekrdsvepgqkylnpqnsl 28

Scoring table:
 PAM 150
 Gap 15

Searched: 142080 segs, 47172406 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: P1r62
 1:plrl 2:plrl2 3:plrl3 4:plrl4

Statistics: Mean 29.032; Variance 38.204; scale 0.760

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	202	100.0	455	1	GQHUT1	tumor necrosis factor 6.35e-36
2	169	83.7	454	2	I57826	tumor necrosis factor 1.19e-26
3	169	83.7	454	1	GOMST1	tumor necrosis factor 1.19e-26
4	167	82.7	461	2	GOMST1	tumor necrosis factor 4.24e-26
5	155	76.7	461	2	UC4302	tumor necrosis factor 8.18e-23
6	74	36.6	213	2	C69980	hypothetical protein 9.88e-03
7	63	31.2	518	2	H70388	selenophosphate synth 1.57e+00
8	63	31.2	506	2	T07942	probable squalene mon 1.57e+00
9	63	31.2	518	2	T07940	probable squalene mon 1.57e+00
10	63	31.2	563	2	S27083	hemagglutinin-inflin 1.57e+00
11	63	31.2	1444	2	S57335	cleavage and polyaden 2.43e+00
12	62	30.7	264	2	S47023	DNA-directed RNA poly 2.43e+00
13	62	30.7	699	2	B72775	probable DNA replicat 2.43e+00
14	62	30.7	916	2	E71330	probable preprotein t 2.43e+00
15	62	30.7	1376	2	S63986	collagen alpha 5 chain 3.73e+00
16	61	30.2	98	2	D30338	exogenous DNA-binding 3.73e+00
17	61	30.2	451	2	E75131	hypothetical protein 3.73e+00
18	61	30.2	563	2	S47095	phr protein - pseudo 3.73e+00
19	61	30.2	837	2	T00355	hypothetical protein 3.73e+00
20	60	29.7	3623	2	T08618	intrinsic ribosomal p 5.70e+00
21	60	29.7	88	2	F70945	probable ribosomal pr 5.70e+00
22	60	29.7	148	2	B43663	host-inducible protei 5.70e+00
23	60	29.7	313	2	H69297	conserved hypothetical 5.70e+00

24	60	29.7	1000	2	JF0110	Dis3p protein - human
25	60	29.7	3034	2	T14119	seven pass transmembr
26	59	28.2	169	2	T04285	hypothetical protein
27	59	29.2	396	2	I75615	mammary tumor integra
28	59	29.2	406	2	S42394	G-box-binding protein
29	59	29.2	636	2	S41067	collagen alpha 1(III)
30	59	29.2	948	2	A34416	hydroxymethylglutaryl
31	59	29.2	1464	2	S59856	collagen alpha 1(III)
32	59	29.2	1466	1	GQHUT1	collagen alpha 1(III)
33	59	29.2	3433	1	GNMVKY	genome polypeptide -
34	58	28.7	97	2	S62625	hydrophobin HFB1 - fu
35	58	28.7	155	2	F69190	conserved hypothetical
36	58	28.7	289	2	B32459	Na+/K+-exchanging ATP
37	58	28.7	290	2	UC5108	Na+/K+-exchanging ATP
38	58	28.7	304	2	I50721	synemin - chicken (fr
39	58	28.7	416	1	KIVKGL	phosphoglycerate kina
40	58	28.7	880	1	B33926	DNA-directed RNA poly
41	58	28.7	1765	2	A31494	DNA-directed RNA poly
42	58	28.7	1766	2	B31875	DNA-directed RNA poly
43	58	28.7	1766	2	A31875	DNA-directed RNA poly
44	58	28.7	3432	1	GNMVKY	genome polypeptide -
45	58	28.7	3432	1	GNMVKY	genome polypeptide -

ALIGNMENTS

RESULT 1
 ENTRY GQHUT1 #type complete
 TITLE tumor necrosis factor receptor 1 precursor - human
 ALTERNATE_NAMES P55 tumor necrosis factor receptor; TNF receptor
 CONTAINS tumor necrosis factor; alpha inhibitor; tumor necrosis factor binding protein 1 (TNF blocking factor)
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Jun-1999

ACCESSIONS
 A38208; A34899; A34900; A36555; C36555; A38281; S12057;
 J070758; A60231; A38256; A60594; A35010; J02404
 A38208

REFERENCE
 #authors Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
 #journal Genomics (1992) 13:219-224
 #title Structure of the human TNF receptor 1 (p60) gene (TNFR1) and localization to chromosome 12p13.
 #cross-references MIM:92250049
 #accession A38208
 ##molecule_type DNA
 ##residues 1-455 #label FUC
 ##cross-references GB:M75864; GB:M75865; GB:M75866; NID:g339748; P1DN:AAA61201.1; P1D:g339750

REFERENCE
 #authors Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslauer, W.
 #journal Cell (1990) 61:351-359
 #title Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor.
 #cross-references MIM:90235284
 #accession A34899
 ##molecule_type mRNA
 ##residues 1-455 #label LOE
 ##cross-references GB:M58286; GB:M33480; NID:g339753; P1DN:AAA36753.1; P1D:g339754
 ##experimental_source placenta
 ##note part of this sequence, including the amino end of the mature protein, confirmed by protein sequencing

REFERENCE
 #authors Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Mory, G.H.W.; Galanaga, T.; Granger, G.A.; Lenz, R.; Raab, H.; Kohr, W.J.; Goeddel, D.V.
 #journal Cell (1990) 61:361-370
 #title Molecular cloning and expression of a receptor for human tumor necrosis factor.
 #cross-references MIM:90235285
 #accession A34900
 ##molecule_type mRNA

Secluded Camp Allotro A

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Query Match      100.0%; Score 202; DB 1; Length 455;
Best Local Similarity 96.4%; Pred. No. 6,35e-36;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db
30 LYPHGLDRERKDSVCPGKYLHPQXNSI 57
1 LYPHGLDRERKDSVCPGKYLHPQXNSI 28

RESULT 2
ENTRY      157826 #type complete
TITLE      tumor necrosis factor receptor - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
23-Jul-1999

ACCESSIONS
REFERENCE   157826
#authors    Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.;
#journal    Mol. Immunol. (1993) 30:165-176
#title      Genomic organization and promoter function of the murine
            tumor necrosis factor receptor beta gene.
#cross-references MIMD:93156721
#accession  157826
#status     preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues   1-454 #label RES
#cross-references GB:M76656; NID:g202100; PID:AAA40465.1; PID:g202102

GENETICS
#gene       TNFR-2
#introns    13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF
               receptor repeat homology
               cytokine receptor

KEYWORDS
FEATURE     44-82 #domain NGF receptor repeat homology #label NGF
SUMMARY     #length 454 #molecular-weight 50030 #checksum 4267

Query Match      83.7%; Score 169; DB 2; Length 454;
Best Local Similarity 78.6%; Pred. No. 1,19e-26;
Matches 22; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db
30 LYPHGLDRERKDSVCPGKYLHPQXNSI 57
1 LYPHGLDRERKDSVCPGKYLHPQXNSI 28

RESULT 3
ENTRY      GONST1 #type complete
TITLE      tumor necrosis factor receptor 1 precursor - mouse
ALTERNATE_NAMES #formal_name Mus musculus #common_name house mouse
ORGANISM       30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
DATE           22-Jun-1999
ACCESSIONS     A38634; B40254; S16677; S19021; I54532
REFERENCE      A38634
#authors       Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice,
               G.C.; Mong, G.H.W.; Chen, E.Y.; Goeddel, D.V.;
               Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834
#journal       Cloning and expression of cDNAs for two distinct murine tumor
               necrosis factor receptors demonstrate one receptor is
               species specific.
               #cross-references MIMD:91187885
#accession     A38634
#molecule_type mRNA
#residues      1-454 #label LEW
#cross-references GB:M0468; NID:g199825; PID:AAA39751.1; PID:g199826

AUTHORS
#journal       Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan,
               C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.
               Mol. Cell. Biol. (1991) 11:3020-3026
#journal       Molecular cloning and expression of the type 1 and type 2
               murine receptors for tumor necrosis factor.

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#cross-references MIMD:91246168
#accession     B40254
#molecule_type mRNA
#residues      1-454 #label GO2
#cross-references GB:M0468; NID:g199825; PID:AAA39751.1; PID:g199826
REFERENCE      S16677
#authors       Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissmerghis,
               A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J.
               Eur. J. Immunol. (1991) 21:1649-1656
#journal       Cloning, expression and cross-linking analysis of the murine
               p55 tumor necrosis factor receptor.
#cross-references MIMD:91285014
#accession     S16677
#molecule_type mRNA
#residues      1-454 #label BAR
#cross-references EMBL:X59238; NID:g53578; PID:CAA41922.1; PID:g53579
REFERENCE      S19021
#authors       Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
#journal       Immunogenetics (1991) 34:338-340
#title         Molecular cloning and expression of the mouse Tnf receptor
               type b.
#cross-references MIMD:92039815
#accession     S19021
#molecule_type mRNA
#residues      1-454 #label ROT
#cross-references EMBL:X57796; NID:g54848; PID:CAA40936.1; PID:g54849
REFERENCE      I54532
#authors       Bebo, B.F.
#journal       Immunogenetics (1994) 39:450-451
#title         Nucleotide sequence of the TNF type I receptor from a mouse
               endothelioma cell line.
#cross-references MIMD:94245292
#accession     I54532
#status        translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues      1-454 #label RES
#cross-references GB:I26349; NID:g430732; PID:AAA59361.1; PID:g430733
COMMENT        This protein is one of two distantly related receptors for both
               TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF
               receptor repeat homology
               duplication; glycoprotein; receptor; transmembrane protein

KEYWORDS
FEATURE     1-29 #domain signal, sequence #status predicted #label SIG\
30-454      #product tumor necrosis factor receptor type 1 #status
               predicted #label MAT\

30-212      #domain extracellular #status predicted #label EXT\
44-82       #domain NGF receptor repeat homology #label NG1\
84-126      #domain NGF receptor repeat homology #label NG2\
127-167     #domain NGF receptor repeat homology #label NG3\
168-204     #domain NGF receptor repeat homology #label NG4\
213-235     #domain transmembrane #status predicted #label MEM\
236-454     #domain intracellular #status predicted #label INT\
54,151,202  #binding_site carbohydrate (Asn) (covalent) #status
               predicted

SUMMARY      #length 454 #molecular-weight 50129 #checksum 4839

Query Match      83.7%; Score 169; DB 1; Length 454;
Best Local Similarity 78.6%; Pred. No. 1,19e-26;
Matches 22; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db
30 LYPHGLDRERKDSVCPGKYLHPQXNSI 57
1 LYPHGLDRERKDSVCPGKYLHPQXNSI 28

RESULT 4
ENTRY      GORT1 #type complete
TITLE      tumor necrosis factor receptor 1 precursor - rat
ALTERNATE_NAMES #formal_name Rattus norvegicus #common_name Norway rat
ORGANISM       30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change
DATE           22-Jun-1999

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ACCESSIONS      B36555
REFERENCE        A36555
#authors        Himmler, A.; Maurer-Fogy, I.; Krenke, M.; Scheurich, P.;
#journal        Strömmer, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
#title          DNA Cell Biol. (1990) 9:705-715
#cross-references M01D:91090841
#accession      B36555
##molecule_type mRNA
##residues      1-461 ##label HIM
#cross-references GB:M63122; NID:g207361; PIDN:AAA42256.1; PID:g207362
COMMENT          This protein is one of two known receptors for both TNF-alpha
                  (cachectin) and TNF-beta (lymphotoxin).
CLASSIFICATION  #superfamily tumor necrosis factor receptor type 1; NGF
                  receptor repeat homology
KEYWORDS         duplication; glycoprotein; receptor; transmembrane protein
FEATURE          1-29
                  30-461
                  30-211
                  30-201
                  44-82
                  84-126
                  127-167
                  168-204
                  212-234
                  235-461
                  54,151,201
SUMMARY          #length 461 #molecular-weight 50969 #checksum 1617
Query Match      82.7%; Score 167; DB 1; Length 461;
Best Local Similarity 78.6%; Pident. No. 4; 2ae-26;
Matches          22; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Db              30 LVPSTGDKREKRDNLCPGKYAHPKNNST 57
                ||| |||||:::||||| || |||
Oy              1 lvphtgdkrekdsvcpqgkylnhpqxnst 28

RESULT          5
ENTRY           JC4302      #type complete
TITLE           tumor necrosis factor receptor p55 precursor - pig
ORGANISM        #formal_name Sus scrofa domestica #common_name domestic pig
DATE            29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change
                23-Jul-1999
ACCESSIONS      JC4302; PC4093
REFERENCE       JC4302
#authors        Suter, B.; Pauli, U.
#journal        Gene (1995) 163:263-266
#title          Cloning of the cDNA encoding the porcine p55 tumor necrosis
                  factor receptor.
#cross-references M01D:96011645
#accession      JC4302
##molecule_type mRNA
##residues      1-461 ##label SUR
#cross-references GB:U19594; NID:g1141752; PIDN:AAC48499.1;
                  PID:g1141753
#accession      PC4093
##molecule_type protein
##residues      1-7 ##label SUR2
#experimental_source kidney cell; line 15

GENETICS        tnfr
CLASSIFICATION  #superfamily tumor necrosis factor receptor type 1; NGF
                  receptor repeat homology
KEYWORDS         glycoprotein; kidney; receptor; transmembrane protein; tumor
FEATURE

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1-29      #domain signal sequence #status predicted #label SIG\
30-461    #product tumor necrosis factor receptor p55 #status
          predicted #label MAF\
44-194     #domain extracellular cysteine rich #status predicted
          #label EXT\
44-82      #domain NGF receptor repeat homology #label NG1\
84-136     #domain NGF receptor repeat homology #label NGF\
211-231    #domain transmembrane #status predicted #label TM\
361-447     #domain signal transduction #status predicted #label
          S/T\
54,145,151 #binding_site carbohydrate (Asn) (covalent) #status
           predicted
SUMMARY    #length 461 #molecular-weight 50696 #checksum 8079

Query Match       76.7%; Score 155; DB 2; Length 461;
Best Local Similarity 75.0%; Pred. No. 8.18e-23;
Matches 21; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Db      30 LVLHPDREKRRESLCPQGYKSHPNQNSI 57
        ||| | | | | | | | | | | | | | | |
        1 LVPHYGRDKRIDSVCPGKYHLPQNXTS 28

RESULT      6
ENTRY
TITLE      C69980      #type complete
ORGANISM   hypothetical protein yrrT - Bacillus subtilis
DATE       05-Dec-1997 #sequence_revision 05-Dec-1997 #text-change
                24-Sep-1998
ACCESSIONS C69980
REFERENCE A69580
AUTHORS    Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.;
Allion, G.; Azevedo, V.; Belloir, M.G.; Bessières, P.;
Bollhot, A.; Borcherdt, S.; Boris, R.J.; Bourcier, L.; Brans,
A.; Braun, M.; Brignell, S.C.; Bron, S.; Broillet, S.;
Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
Choi, S.K.; Codani, J.J.; Conerton, I.F.; Cummings, N.J.;
Daniel, K.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;
Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
M.; Fujita, Y.; Fuma, S.; Gallizi, A.; Galleron, N.; Glum,
S.Y.; Glaeser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.;
Gulsept, G.; Guy, B.-J.; Haga, A.; Halech, J.; Harwood,
C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;
Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karimata, D.;
Kasahara, Y.; Kleier-Blanchard, M.; Klein, C.; Kobayashi,
Y.; Koetter, P.; Kontagstein, G.; Krogh, S.; Kumano, M.;
Kurita, K.; Lapidus, A.; Lardinols, S.; Lauber, J.;
Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.;
Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno,
M.; Moestl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly,
M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro,
V.; Poll, T.M.; Portetalle, D.; Porwollik, S.; Prescott,
A.M.; Presecan, E.; Puigc, P.; Punelle, B.; Rapoport, G.;
Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.;
Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, E.;
Schleisch, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.;
Sekowska, A.; Seror, S.J.; Serrou, P.; Shin, B.S.; Soldo,
B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.;
Takemaru, K.; Takeuchi, M.; Tanakoshi, A.; Tanaka, T.;
Tejparva, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.;
Vandenolt, M.; Vannier, F.; Vasaroth, A.; Viart, A.;
Wambutt, R.; Wedler, E.; Wedler, H.; Welteneberger, T.;
Winiers, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto,
Y.; Yata, K.; Yoshida, K.; Yoshioka, H.F.; Zumbach, E.;
Yoshikawa, H.; Danchin, A.
Nature (1997) 390:249-256
The complete genome sequence of the Gram-positive bacterium
Bacillus subtilis.
#cross-references NCBI:98044033
#accession C69980
#status preliminary; nucleic acid sequence not shown;
translation not shown

```

```
##molecule-type DNA
##residues 1-213 ##label KUN
##cross-references GB:Z99117; GB:Al009126; NID:g2634966; PID:e1183958;
##experimental_source strain 168
PID:g2635174
GENETICS
#gene
#introns
#exons
#length 213 #molecular-weight 24196 #checksum 2669
SUMMARY
Query Match 36.6%; Score 74; DB 2; Length 213;
Best Local Similarity 40.0%; Pred. No. 9.88e+03;
Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
Db 119 HLTDEKRAIKYGTIHLHDKY 143
QY 4 hlgdrekrdsvcpqkyihpqxnsi 28

RESULT 7
ENTRY H70388 #type complete
TITLE selenophosphate synthase - Aquifex aeolicus
ALTERNATE_NAMES #formal_name Aquifex aeolicus
ORGANISM 08-May-1998 #sequence_revision 08-May-1998 #text_change
DATE 08-May-1998
ACCESSIONS H70388
REFERENCE A70300
AUTHORS Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.;
Lenox, A.L.; Graham, D.E.; Overbeek, R.; Sneed, M.A.;
Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short,
J.M.; Olson, G.J.; Swanson, R.V.
#journal Nature (1998) 392:353-358
#title The complete genome of the hyperthermophilic bacterium
#accession Aquifex aeolicus.
#cross-references M01D:98196666
#status preliminary; nucleic acid sequence not shown;
#molecule-type DNA translation not shown
#residues 1-311 ##label AQF
##cross-references GB:AE000719; NID:g2983517; PID:g2983519; GB:AE000657
##experimental_source strain VFS
GENETICS
#gene
#introns
#exons
#length 311 #molecular-weight 34231 #checksum 842
SUMMARY
Query Match 31.2%; Score 63; DB 2; Length 311;
Best Local Similarity 66.7%; Pred. No. 1.57e+00;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Db 122 GICPEGKTY 130
QY 13 svcpqkyi 21

RESULT 8
ENTRY T07942 #type complete
TITLE probable squalene monooxygenase (EC 1.14.99.7) Sqp1 - rape
ALTERNATE_NAMES #formal_name Brassica napus #common_name rape
ORGANISM 21-May-1999 #sequence_revision 21-May-1999 #text_change
DATE 11-Jun-1999
ACCESSIONS T07942
REFERENCE Z16234
AUTHORS Schaefer, U.A.; Reed, D.W.; Hunter, D.G.; Yao, K.; Weninger,
A.M.; Tsang, E.W.T.; Reaney, M.J.T.; Mackenzie, S.L.;
Covello, P.S.
#journal Plant Mol. Biol. (1999) 39:721-728
#title An example of intron junctional sliding in the gene families
#accession encoding squalene monooxygenase homologues in Arabidopsis
#status preliminary
#molecule-type mRNA translated from GB/EMBL/DBJ

##residues 1-506 ##label SCH
##cross-references EMBL:A005931; NID:e1291750; PID:e1291751
##experimental_source cv. Westar; developmental stage:
greenling-retiolated; tissue type: shoots
GENETICS
#gene
#introns
#exons
#length 506 #molecular-weight 55571 #checksum 5540
SUMMARY
Query Match 31.2%; Score 63; DB 2; Length 506;
Best Local Similarity 30.0%; Pred. No. 1.57e+00;
Matches 6; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
Db 74 HYERDMREPRVMMGEFMP 93
QY 4 hlgdrekrdsvcpqkyihp 23

RESULT 9
ENTRY T07940 #type complete
TITLE probable squalene monooxygenase (EC 1.14.99.7) Sqp2 - rape
ALTERNATE_NAMES #formal_name Brassica napus #common_name rape
ORGANISM 21-May-1999 #sequence_revision 21-May-1999 #text_change
DATE 11-Jun-1999
ACCESSIONS T07940
REFERENCE Z16234
AUTHORS Schaefer, U.A.; Reed, D.W.; Hunter, D.G.; Yao, K.; Weninger,
A.M.; Tsang, E.W.T.; Reaney, M.J.T.; Mackenzie, S.L.;
Covello, P.S.
#journal Plant Mol. Biol. (1999) 39:721-728
#title An example of intron junctional sliding in the gene families
#accession encoding squalene monooxygenase homologues in Arabidopsis
#status preliminary
#molecule-type mRNA translated from GB/EMBL/DBJ
#residues 1-518 ##label SCH
##cross-references EMBL:A005928; NID:e1291748; PID:e1291749
##experimental_source cv. Westar; developmental stage:
greenling-retiolated; tissue type: shoots
GENETICS
#gene
#introns
#exons
#length 518 #molecular-weight 57399 #checksum 7018
SUMMARY
Query Match 31.2%; Score 63; DB 2; Length 518;
Best Local Similarity 30.0%; Pred. No. 1.57e+00;
Matches 6; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
Db 75 HYERDMREPRVMMGEFMP 94
QY 4 hlgdrekrdsvcpqkyihp 23

RESULT 10
ENTRY S22083 #type complete
TITLE hemagglutinin - Influenza A virus
ALTERNATE_NAMES #formal_name Influenza A virus
ORGANISM 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
DATE 20-Sep-1999
ACCESSIONS S22083
REFERENCE S22083
AUTHORS Garten, W.D.
#journal submitted to the EMBL Data Library, May 1992
#accession #status
#molecule-type DNA preliminary
#residues 1-563 ##label GAR
#cross-references EMBL:U12617; NID:g60497; PID:CAA78263.1; PID:g60498
#superfamily Influenza virus hemagglutinin
#length 563 #molecular-weight 62883 #checksum 792
```


##molecule_type DNA
 ##residues 1-916 ##label COL
 ##cross-references GB:AE001217; GB:AE000520; NID:G3322656;
 PIDN:ACG5365.1; PID:G3322659
 ##experimental_source strain Nichols

GENETICS

#gene TP0379

CLASSIFICATION #superfamily preprotein translocase secA; DEAD/H box helicase

homology

KEYWORDS ATP; P-loop

FEATURE

103-599 #domain DEAD/H box helicase homology #label DEAD\
 103-110 #region nucleotide-binding motif A (P-loop)\
 206-211 #region nucleotide-binding motif B\
 210-213 #region DEAD/H motif #status atypical
 #length 916 #molecular-weight 103779 #checksum 4056

SUMMARY

Query Match 30.7%; Score 62; DB 2; Length 916;
 Best Local Similarity 25.9%; Pred. No. 2.43e+00;
 Matches 7; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Db 433 VYI5EEKWSAICDEIKEAHTKQPV 459

QY 2 vphlgdrekrdsvcpqgkyihpqnsl 28

RESULT 15

ENTRY 15 S63986 #type fragment

TITLE collagen alpha 5 chain - sea urchin (Strongylocentrotus

purpuratus) (fragment)

ORGANISM #formal_name Strongylocentrotus purpuratus #common_name

purple urchin

DATE 20-Jul-1996 #sequence_revision 08-Nov-1996 #text_change

25-Apr-1997

ACCESSIONS S63986; S64638

REFERENCE S63985

#authors Exposito, J. Y.; Boure, N.; Delage, G.; Garrone, R.

#journal Eur. J. Biochem. (1995) 234:55-65

#title Characterization of two genes coding for a similar

four-cysteine motif of the amino-terminal propeptide of a

sea urchin fibillar collagen.

#cross-references MVID:96096722

#accession S63986

##status nucleic acid sequence not shown

##molecule_type DNA

##residues 1-1376 #label EXP

##cross-references EMBL:X83804

REFERENCE S64637

#authors Exposito, J. Y.

#submission submitted to the EMBL Data Library, July 1995

#accession S64638

#molecule_type DNA

1-658, 'G', 660-870, 'G', 872-901, 'H', 903-1185, 'T',

1187-1214, 'Y', 1216-1376 #label EXM

##cross-references EMBL:X83804

GENETICS

#gene COLP5alpha

#introns 73/1; 136/2; 221/1; 369/1; 517/1; 659/1; 799/1; 948/1;

1093/1; 1236/1

CLASSIFICATION #superfamily von Willebrand factor type C repeat homology

KEYWORDS extracellular matrix

FEATURE

15-73

SUMMARY #domain von Willebrand factor type C repeat homology

#label VMC

#length 1376 #checksum 7553

Query Match 30.7%; Score 62; DB 2; Length 1376;

Best Local Similarity 38.5%; Pred. No. 2.43e+00;

Matches 10; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Db 890 FVPLVTNFDMDLCKPOVKTCNEVN 915

QY 1 lvphlgdrekrdsvcpqgkyihpqn 26

Search completed: Tue Apr 18 11:06:48 2000
 Job time : 53 secs.

 M P E R S I O N
 (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Tue Apr 18 11:07:05 2000; Maspar time 27.80 Seconds
 Tabular output not generated. 30.077 Million cell updates/sec

Title: >PEP1.PEP
 Description: (1-28) from new.pep
 Perfect Score: 202
 Sequence: 1 lvphlgdrekidsvcpgqkyihpqxst 28

Scoring table:
 PAM 150
 Gap 15

Searched: 82229 seqs, 29864866 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot38
 1:swissprot

Statistics: Mean 29.784; Variance 34.076; scale 0.874

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	202	100.0	455	1	TNRI_HUMAN	2.05e-41
2	169	83.7	454	1	TNRI_MOUSE	8.20e-31
3	167	82.7	461	1	TNRI_MOUSE	3.50e-30
4	155	76.7	461	1	TNRI_RAT	1.98e-26
5	63	31.2	336	1	SELD_AQUAE	3.94e-01
6	63	31.2	1442	1	CPSA_HUMAN	3.94e-01
7	62	30.7	1444	1	CPSA_BOVIN	6.40e-01
8	62	30.7	264	1	SECA_TREPA	6.40e-01
9	61	30.2	916	1	SECA_TREPA	6.40e-01
10	61	30.2	98	1	COMG_OPERON	1.03e+00
11	60	29.7	148	1	MOD_RHIFR	1.66e+00
12	59	29.2	140	1	YB18_SCHPO	2.65e+00
13	59	29.2	445	1	INT6_MOUSE	2.65e+00
14	59	29.2	473	1	PSST_HUMAN	2.65e+00
15	59	29.2	568	1	G6P1_CLAMI	2.65e+00
16	59	29.2	636	1	CA13_RAT	2.65e+00
17	59	29.2	948	1	HMDH_SCHMA	2.65e+00
18	59	29.2	1464	1	CA13_MOUSE	2.65e+00
19	59	29.2	1466	1	CA13_HUMAN	2.65e+00
20	59	29.2	3433	1	POLG_KUNJM	2.65e+00
21	58	28.7	97	1	HYPI_TRIRE	4.20e+00
22	58	28.7	290	1	ATNC_BOVIN	4.20e+00
23	58	28.7	290	1	ATNC_HUMAN	4.20e+00

24	58	28.7	290	1	ATNC_MOUSE	4.20e+00
25	58	28.7	490	1	ATNC_RAT	4.20e+00
26	58	28.7	216	1	PKR_KLULA	4.20e+00
27	58	28.7	569	1	G6P2_GIARO	4.20e+00
28	58	28.7	570	1	G6P1_GIARO	4.20e+00
29	58	28.7	683	1	PILO1_SCHPO	4.20e+00
30	58	28.7	880	1	IFP2_SCHPO	4.20e+00
31	58	28.7	1079	1	IFP2_SCHPO	4.20e+00
32	58	28.7	1766	1	RPB2_TRYBB	4.20e+00
33	58	28.7	1766	1	RPB1_TRYBB	4.20e+00
34	58	28.7	3432	1	POLG_JAEVJ	4.20e+00
35	58	28.7	3432	1	POLG_JAEVJ	4.20e+00
36	58	28.7	3432	1	POLG_JAEVJ	4.20e+00
37	57	28.2	377	1	TYXN_BACSV	6.61e+00
38	57	28.2	469	1	DPD2_BOVIN	6.61e+00
39	57	28.2	476	1	U136_HCMVA	6.61e+00
40	57	28.2	698	1	TRFE_YEAST	6.61e+00
41	57	28.2	827	1	RAPI_YEAST	6.61e+00
42	57	28.2	859	1	PMS2_MOUSE	6.61e+00
43	57	28.2	862	1	PMS2_HUMAN	6.61e+00
44	57	28.2	1210	1	EGFR_HUMAN	6.61e+00
45	56	27.7	568	1	G6P1_CLAYA	1.03e+01

ALIGNMENTS

RESULT ID	1	STANDARD:	PRT:	455 AA.
AC	PI9438;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR			
DE	BINDING PROTEIN 1) (TBP1) (P60) (TNF-R1) (P95) (CD120A).			
GN	TNFRSF1A OR TNFR1 OR TNFR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Homidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=PLACENTA;			
RC	MEDLINE: 90235285.			
RX	SCHALL T.J., LEWIS M., KOLLER K.J., LEE A., RICE G.C., WONG G.H.W.,			
RA	GETANAGA T., GRANGER G.A., LEMTZ R., RAAB H., KOHR W.J., GOEDDEL D.V.,			
RT	"Molecular cloning and expression of a receptor for human tumor			
RT	necrosis factor."			
RL	Cell 61:361-370(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE: 90235284.			
RX	LOETSCHER H., PAN Y.-C.E., LAHM H.-W., GENTZ R., BROCKHAUS M.,			
RA	TABUCHI H., LESSLAUER W.,			
RT	"Molecular cloning and expression of the human 55 kd tumor necrosis			
RT	factor receptor."			
RL	Cell 61:351-359(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE: 91090821.			
RX	NOPIAR Y., KEMPER O., BRAKEBUSCH C., ENGELMANN H., ZWANG R.,			
RA	ADDERA D., HOLTMANN H., WALLACH D.,			
RT	"Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA			
RT	for the type I TNF-R, cloned using amino acid sequence data of its			
RT	soluble form, encodes both the cell surface and a soluble form of the			
RT	receptor."			
RL	EMBO J. 9:3269-3278(1990).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE: 91090841.			
RX	HIMMER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., FITZENMAIER K.,			
RA	LANZ M., OLSSON I., HADPTMANN R., STATOVA C., ADOLF G.R.,			
RT	"Molecular cloning and expression of human and rat tumor necrosis			
RT	factor receptor chain (p60) and its soluble derivative, tumor			
RT	necrosis factor-binding protein."			

RN DNA Cell Biol. 9:705-715(1990).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RX MEDLINE: 91017509.
 RA GRAY P.W., BARRETT K., CHANTREY D., TURNER M., FELDMAN M.;
 RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and
 expression of recombinant soluble TNF-binding protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92250049.
 RA FUCHS P., STREHL S., DWORZAK M., HIMMLER A., AMEROS P.F.;
 RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
 localization to chromosome 12p13.";
 RL Genomics 13:219-224(1992).
 RN [7]
 RP SEQUENCE OF 41-45.
 RX MEDLINE: 90110215.
 RA ENGELMANN H., NOVICK D., WALLACH D.;
 RT "Two tumor necrosis factor-binding proteins purified from human
 urine. Evidence for immunological cross-reactivity with cell surface
 tumor necrosis factor receptors.";
 RL J. Biol. Chem. 265:1531-1536(1990).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.
 RX MEDLINE: 93258809.
 RA BANNER D.W., D'ARCY A., JAMES W., GENTZ R., SCHOENFELD H.-J.,
 RA BROGER C., LOESCHER H., LESSLAUER W.;
 RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
 beta complex: implications for TNF receptor activation.";
 RL Cell 73:431-445(1993).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
 RX MEDLINE: 97094982.
 RA NAISWITZ J.H., DEVINE T.O., KHONO H., SPRANG S.R.;
 RT "Structures of the extracellular domain of the type I tumor necrosis
 factor receptor.";
 RL Structure 4:1251-1262(1996).
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE PADD
 RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
 AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
 PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
 SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
 PROTEASES) MEDIATING APOPTOSIS. CONTRIBUTES TO THE INDUCTION OF
 NONCYTOTOXIC TNF EFFECTS INCLUDING ANTI-VIRAL STATE AND ACTIVATION
 OF THE ACID SPHINGOMYELINASE.
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 NF-KAPPA B SIGNALING.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO
 THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH
 NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD120a entry;
 WWW-http://www.ncbi.nlm.nih.gov/prov/ncbi/cd120a.htm".
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: X55313; CAA39021.1;
 CC EMBL: M33294; AAA03210.1; -
 CC DR

DR EMBL: M58286; AAA36753.1; -
 DR EMBL: M63121; AAA36754.1; -
 DR EMBL: M75866; AAA61201.1; -
 DR EMBL: M75864; AAA61201.1; JOINED.
 DR EMBL: M75865; AAA61201.1; JOINED.
 DR EMBL: M60275; AAA36756.1; -
 DR EMBL: A21522; CAA01558.1; -
 DR PIR: A34899; GOH071.
 DR PIR: A35010; A35010.
 DR PIR: S12057; S12057.
 DR PIR: A38208; A38208.
 DR PDB: ITNR; 3I-JUL-94.
 DR PDB: INCF; 07-DEC-95.
 DR PDB: IEXT; 11-JAN-97.
 DR MIM: 191190; -
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS00050; TNFR_NGFR_2; 3.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR PFAM: PF00020; TNFR_C6; 4.
 DR PFAM: PF00531; death; 1.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis;
 KW 3d-structure.
 FT SIGNAL 1 21
 FT CHAIN 22 455
 FT CHAIN 41 291
 FT DOMAIN 22 211
 FT TRANSMEM 212 234
 FT DOMAIN 235 455
 FT DOMAIN 43 196
 FT REPEAT 43 82
 FT REPEAT 83 125
 FT REPEAT 126 166
 FT REPEAT 167 196
 FT DOMAIN 338 348
 FT DOMAIN 356 441
 FT DISULFID 44 58
 FT DISULFID 59 72
 FT DISULFID 62 81
 FT DISULFID 84 99
 FT DISULFID 102 117
 FT DISULFID 105 125
 FT DISULFID 127 143
 FT DISULFID 146 158
 FT DISULFID 149 166
 FT DISULFID 168 179
 FT DISULFID 182 191
 FT DISULFID 185 195
 FT CARBOHYD 54 54
 FT CARBOHYD 145 145
 FT CARBOHYD 151 151
 FT CARBOHYD 412 412
 FT CONFLICT 443 446
 FT CONFLICT 443 446
 SQ SEQUENCE 455 AA; 50494 MW; CED0A05F CRC32;
 Query Match 100.0%; Score 202; DB 1; Length 455;
 Best Local Similarity 96.4%; Pred. No. 2.05e-41;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 30 LYPHLDGDRKRDVYCPGKTIHPQNNST 57
 QY 1 LYPHLDGDRKRDVYCPGKTIHPQNNST 28
 RESULT 2
 ID TNFR1_MOUSE STANDARD; PRT; 454 AA.
 AC P25118;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
 GN TNFRSF1A OR TNFR1 OR TNFR-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91187885.
 RA LEWIS M., TARAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
 RA WONG G.H., CHEN E.Y., GOEDDEL D.V.,
 RT "Cloning and expression of cDNAs for two distinct murine tumor
 RT necrosis factor receptors demonstrate one receptor is species
 RT specific."
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91246168.
 RA GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,
 RA COPELAND N.G., JENKINS N.A., SMITH C.A.,
 RT "Molecular cloning and expression of the type 1 and type 2 murine
 RT receptors for tumor necrosis factor."
 RL Mol. Cell. Biol. 11:3020-3026(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91285014.
 RA BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P., KISSONERGHIS A.M.,
 RA GRAY P.W., FELDMANN M., FOXWELL B.M.J.,
 RT "Cloning, expression and cross-linking analysis of the murine p55
 RT tumor necrosis factor receptor."
 RL Eur. J. Immunol. 21:1649-1656(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX TISSUE-SPLEEN;
 RX MEDLINE; 92059815.
 RA ROTHE J.G., BROCKHAUS M., GENTZ R., LESSLAUER W.,
 RT "Molecular cloning and expression of the mouse Tnf receptor type b."
 RL Immunogenetics 34:338-340(1991).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94245232.
 RA BEBO B.F., LINTHICUM D.S.,
 RT "Nucleotide sequence of the TNF type I receptor from a mouse
 RT endothelioma cell line."
 RL Immunogenetics 39:450-451(1994).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93156721.
 RA ROTHE J., BLUTHMANN H., GENTZ R., LESSLAUER W., STEINMETZ M.,
 RT "Genomic organization and promoter function of the murine tumor
 RT necrosis factor receptor beta gene."
 RL Mol. Immunol. 30:165-175(1993).
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
 CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
 CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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 CC EMBL; M60468; AAA39751.1; -

DR EMBL; M59377; AAA40464.1; -
 DR EMBL; X59238; CAA41922.1; -
 DR EMBL; X57796; CAA40936.1; -
 DR EMBL; L26349; AAA59361.1; -
 DR EMBL; M76656; AAA40465.1; -
 DR EMBL; M88067; AAA40465.1; JOINED
 DR EMBL; M76655; AAA40465.1; JOINED
 DR PIR; A386534; GOMSTL.
 DR PIR; S16677; S16677.
 DR PIR; S19021; S19021.
 DR HSSP; P19438; IEXT.
 DR MGI; MGI:1314884; TNFRSF1A.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PROSITE; PS50050; TNFR_NGFR_2; 3.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PFAM; PF00020; TNFR_c6; 4.
 DR PFAM; PF00531; death; 1.
 KM Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
 FT SIGNAL 1 21
 FT CHAIN 22 454
 FT DOMAIN 22 212
 FT TRANSMEM 213 235
 FT DOMAIN 236 454
 FT DOMAIN 43 196
 FT REPEAT 43 82
 FT REPEAT 83 125
 FT REPEAT 126 166
 FT REPEAT 167 196
 FT REPEAT 197 349
 FT DOMAIN 356 441
 FT DISULFID 44 58
 FT DISULFID 59 72
 FT DISULFID 62 81
 FT DISULFID 84 99
 FT DISULFID 102 117
 FT DISULFID 105 125
 FT DISULFID 127 143
 FT DISULFID 146 158
 FT DISULFID 149 166
 FT DISULFID 168 179
 FT DISULFID 182 191
 FT DISULFID 185 195
 FT CARBOHYD 54 54
 FT CARBOHYD 151 151
 FT CARBOHYD 202 202
 FT CONFLICT 394 394
 SQ SEQUENCE 454 AA; 50129 MW; 486EC09 CRC32;
 Query Match 83.7%; Score 169; DB 1; Length 454;
 Best Local Similarity 78.6%; Pred. No. 8, 20e-31;
 Matches 22; Conservativity 3; Mismatches 3; Indels 0; Gaps 0;
 DB 30 LVPSTGLDREKRDSDLPCKGVYHKKNSI 57
 QY 1 LYPHIGDREKRDSDLPCKGVYHKKNSI 28
 ID TNFR1_RAT STANDARD; PRT; 461 AA.
 AC P22934;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
 GN TNFRSF1A OR TNFR1 OR TNFR-1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91090841.
 RA HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,
 RA LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;

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RT      "Molecular cloning and expression of human and rat tumor necrosis
RT      factor receptor chain (p60) and its soluble derivative, tumor
RT      necrosis factor-binding protein."
RT      DNA Cell Biol. 9:705-715(1990).
CC      -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC      RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC      AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC      PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC      SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC      PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC      -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC      HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC      PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC      WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC      PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC      TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC      ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC      NF-KAPPA B SIGNALING (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC      -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC      -----
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CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL: M63122; AAAA2256.1; -.
DR      PIR: B36353; B36353.
DR      HSSP: P19438; 1TNR.
DR      PROSITE: PS00652; TNFR_NGFR_1; 3.
DR      PROSITE: PS50050; TNFR_NGFR_2; 3.
DR      PROSITE: PS50017; DEATH_DOMAIN; 1.
DR      PFM: PF00020; TNFR_C6; 4.
DR      PFM: PF00531; death; 1.
KW      Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
FT      CHAIN          1          21
FT      DOMAIN        22         461
FT      TRANSMEM      212        234
FT      DOMAIN        235        461
FT      DOMAIN        43         196
FT      REPEAT        43         82
FT      REPEAT        83        125
FT      REPEAT        126        166
FT      REPEAT        167        196
FT      REPEAT        197        344
FT      DOMAIN        344        448
FT      DOMAIN        44         58
FT      DISULFID      59         72
FT      DISULFID      62         81
FT      DISULFID      84         99
FT      DISULFID      102        117
FT      DISULFID      105        125
FT      DISULFID      127        143
FT      DISULFID      146        158
FT      DISULFID      149        166
FT      DISULFID      168        179
FT      DISULFID      182        191
FT      DISULFID      185        195
FT      CARBOHYD      54         54
FT      CARBOHYD      151        151
FT      CARBOHYD      201        201
SQ      SEQUENCE      461 AA; 50969 MW; 82f68B08 CRC32;
DB      Query Match      82.7%; Score 167; DB 1; Length 461;
DB      Best Local Similarity 78.6%; Pred. No. 3,50e-30;
DB      Matches 22; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Oy      1 lvpghdrekrdsvcpqgkyihpqxns1 28
RESULT  4
ID      TNFR1_PIG      STANDARD;      PRT;      461 AA.
AC      P50555;
DT      01-OCT-1996 (rel. 34, Created)
DT      01-OCT-1996 (rel. 34, Last sequence update)
DT      15-JUL-1999 (rel. 38, Last annotation update)
DE      TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN      TNFRSF1A OR TNFR1.
OS      Sus scrofa (pig).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC      Eutheria; Cetartiodactyla; Suidae; Sus.
CC      [1]
CC      SEQUENCE FROM N.A.
CC      TISSUE-KIDNEY.
CC      MEDLINE: 96011645.
CC      RA      SUTER B., PAULI U.H.;
CC      RT      "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor
CC      receptor."
CC      RL      Gene 163:263-266(1995).
CC      -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC      RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC      AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC      PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC      SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC      PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC      -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC      HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC      PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC      WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC      PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC      TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC      ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC      NF-KAPPA B SIGNALING (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC      -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC      -----
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CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL: U19994; AAC48499.1; -.
DR      HSSP: P19438; 1TNR.
DR      PROSITE: PS00652; TNFR_NGFR_1; 3.
DR      PROSITE: PS50050; TNFR_NGFR_2; 2.
DR      PROSITE: PS50017; DEATH_DOMAIN; 1.
DR      PFM: PF00020; TNFR_C6; 3.
DR      PFM: PF00531; death; 1.
KW      Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
FT      CHAIN          1          21
FT      DOMAIN        22         461
FT      TRANSMEM      212        233
FT      DOMAIN        234        461
FT      DOMAIN        43         195
FT      REPEAT        43         82
FT      REPEAT        83        125
FT      REPEAT        126        166
FT      REPEAT        167        195
FT      REPEAT        196        350
FT      DOMAIN        340        447
FT      DISULFID      44         58
FT      DISULFID      59         72
FT      DISULFID      62         81
FT      DISULFID      84         99
FT      DISULFID      102        117
FT      DISULFID      105        125
SQ      SEQUENCE      461 AA; 50969 MW; 82f68B08 CRC32;
DB      Query Match      82.7%; Score 167; DB 1; Length 461;
DB      Best Local Similarity 78.6%; Pred. No. 3,50e-30;
DB      Matches 22; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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FT DISULFID 127 143 BY SIMILARITY.
 FT DISULFID 146 158 BY SIMILARITY.
 FT DISULFID 149 166 BY SIMILARITY.
 FT DISULFID 168 179 BY SIMILARITY.
 FT DISULFID 182 190 BY SIMILARITY.
 FT DISULFID 185 194 BY SIMILARITY.
 FT CARBOHYD 54 54 POTENTIAL.
 FT CARBOHYD 86 86 POTENTIAL.
 FT CARBOHYD 145 145 POTENTIAL.
 FT CARBOHYD 151 151 POTENTIAL.
 SQ SEQUENCE 461 AA; 50696 MW; 8E2C350A CRC32;
 Query Match 76.7%; Score 155; DB 1; Length 461;
 Best Local Similarity 75.0%; Pred. No. 1,98e-26;
 Matches 21; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Db 30 LVLHPGDRKRESICPGKXSHPNR51 57
 1 lvphtgdrkresicpgkxshpnr51 28
 RESULT 5
 ID SELD_AQUAE STANDARD; PRT; 336 AA.
 AC 067139;
 DT 15-DEC-1999 (Rel. 39, Created)
 DT 15-DEC-1999 (Rel. 39, Last sequence update)
 DE SELENIUM DONOR DINKINASE (EC 2.7.9.3) (SELENOSELENIUM SYNTHETASE)
 GN SELD OR AQ_1030.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificales; Aquificaceae; Aquifex.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-VF5;
 RA MEDLINE; 98196666.
 RA DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
 RA GRAHAM D.E., OVERBECK R., SNEAD M.A., KELLER M., AUCAY M., HUBER R.,
 RA FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
 RT "THE COMPLETE GENOME OF THE HYPERTHERMOPHILIC BACTERIUM Aquifex
 RT aeolicus";
 RL Nature 392:353-358(1998).
 RN [2]
 RP CONCEPTUAL TRANSLATION.
 RA BAIROCH A.;
 RL Unpublished observations (JUL-1999).
 CC -1- FUNCTION: SYNTHESIZES SELENOSELENIUM FROM SELENIUM AND ATP
 CC (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + SELENIUM + H(2)O -> AMP + SELENOSELENIUM
 CC + PHOSPHATE.
 CC -1- COFACTOR: REQUIRES MAGNESIUM (BY SIMILARITY).
 CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A UGA STOP CODON HAD TO
 CC BE SKIPPED IN POSITION 13 TO PRODUCE THIS ORF. WE (REF.2) BELIEVE
 CC THAT THIS RESIDUE IS MOST PROBABLY AN ACTIVE-SITE SELENOCYSTEINE.
 CC -1- SIMILARITY: BELONGS TO THE SELENOSELENIUM SYNTHETASE 1 FAMILY.
 CC CLASS 1 SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; AEO00719; AAC07095.1; ALT_FRAME.
 DR TRANSFERASE; Selenium; Magnesium; ATP-binding; Selenocysteine.
 KW ACT_SITE 13 13 POTENTIAL.
 FT SE_SITE 13 13 POTENTIAL.
 FT SITE 16 16 IMPORTANT FOR CATALYTIC ACTIVITY (BY
 FT SIMILARITY).
 FT NP_BIND 222 228 ATP (POTENTIAL).

SQ SEQUENCE 336 AA; 36809 MW; 297029FE CRC32;
 Query Match 31.2%; Score 63; DB 1; Length 336;
 Best Local Similarity 66.7%; Pred. No. 3,94e-01;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Db 147 GICEPGKX 155
 13 svcpqgkx 21
 RESULT 6
 ID CP5A_HUMAN STANDARD; PRT; 1444 AA.
 AC Q10570;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 160 KD SUBUNIT (CP5F
 DE 160 KD SUBUNIT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96067159.
 RA MURPHY K.G., MANLEY J.L.;
 RT "The 160-kD subunit of human cleavage-polyadenylation specificity
 RT factor coordinates pre-mRNA 3'-end formation.";
 RL Genes Dev. 9:2672-2683(1995).
 CC -1- FUNCTION: CP5F PLAYS A KEY ROLE IN PRE-MRNA 3'-END FORMATION.
 CC RECOGNIZING THE AAUAA SIGNAL, SEQUENCE AND INTERACTING WITH
 CC POLY(A) POLYMERASE AND OTHER FACTORS TO BRING ABOUT CLEAVAGE AND
 CC STEP OF THE POLYADENYLATION REACTION.
 CC -1- SUBUNIT: CP5F IS A HETEROTETRAMER COMPOSED OF FOUR DISTINCT
 CC SUBUNITS 160, 100, 70 AND 30 KD.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS.
 CC -1- PTM: THE N-TERMINUS IS BLOCKED.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U37012; AAC50293.1;
 DR NUCLEAR protein; RNA-binding. NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 KW DOMAIN 893 908
 FT SEQUENCE 1442 AA; 160822 MW; 8296E75B CRC32;
 SQ
 Query Match 31.2%; Score 63; DB 1; Length 1442;
 Best Local Similarity 28.6%; Pred. No. 3,94e-01;
 Matches 8; Conservative 11; Mismatches 8; Indels 1; Gaps 1;
 Db 1047 IPMTGKEKEFTIENDERYHPQENAF 1074
 2 vphlgdrekrdsvcpqgkxshpnr51 28
 RESULT 7
 ID CP5A_BOVIN STANDARD; PRT; 1444 AA.
 AC Q10569;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 160 KD SUBUNIT (CP5F
 DE 160 KD SUBUNIT).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 OC Bovinae; Bos.

```

RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE-THYMUS;
RX MEDLINE: 9538027.
RA JENNY A., KELLER W.;
RT "Cloning of cDNAs encoding the 160 kDa subunit of the bovine cleavage
RL and polyadenylation specificity factor".
RL Nucleic Acids Res. 23:2629-2635(1995).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE: 92097544.
RA KELLER W., BIENROTH S., LANG K.M., CHRISTOFORI G.;
RT "Cleavage and polyadenylation factor CPF specifically interacts with
RL the pre-mRNA 3' processing signal AAUAAA.".
RL EMBL J. 10:4241-4249(1991).
CC -1- FUNCTION: CPSE PLAYS A KEY ROLE IN PRE-MRNA 3'-END FORMATION,
CC RECOGNIZING THE AAUAAA SIGNAL SEQUENCE AND INTERACTING WITH
CC POLY(A) POLYMERASE AND OTHER FACTORS TO BRING ABOUT CLEAVAGE AND
CC POLY(A) ADDITION. THIS SUBUNIT IS INVOLVED IN THE RNA RECOGNITION
CC STEP OF THE POLYADENYLATION REACTION.
CC -1- SUBUNIT: CPSE IS A HETEROTETRAMER COMPOSED OF FOUR DISTINCT
CC SUBUNITS 160, 100, 70 AND 30 KD.
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOPLASM.
CC -1- PFM: THE N-TERMINUS IS BLOCKED.
CC -----
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CC -----
DR EMBL: X83097; CAA58152.1;
KW Nuclear protein; RNA-binding.
FT DOMAIN 894 909 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
SQ SEQUENCE 1444 AA; 161214 MW; AC11D659 CRC32;

Query Match 31.2%; Score 63; DB 1; Length 1444;
Best Local Similarity 28.6%; Pred. No. 3 94e-01;
Matches 8; Conservative 11; Mismatches 8; Indels 1; Gaps 1;

Db 1048 VERMTEGEEKETTERDERVHPQOEF 1075
OY 2 vphlgdrektr-davcpqgyihpqnsl 28

RESULT 8
ID RPOD-SULAC STANDARD; PRT; 264 AA.
AC P39471;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE DNA-DIRECTED RNA POLYMERASE SUBUNIT D (Ec 2.7.7.6).
GN RPOD.
OS Sulfolobus acidocaldarius.
OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DSM 639;
RX LANGER D., HAIN J., THURIAUX P., ZILLIG W.;
RT "Transcription in archaea: similarity to that in eucarya.".
RT Proc. Natl. Acad. Sci. U.S.A. 92:5768-5772(1995).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE +
CC RNA(N).
CC -1- SUBUNIT: THE S ACIDOCALDIARIUS RNAP IS COMPOSED OF 13 SUBUNITS.
CC -1- SIMILARITY: BELONGS TO THE RPB3/RPC5 RNA POLYMERASE SUBUNIT
CC FAMILY.
CC -----

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CC -----
DR EMBL: X80194; CAA56480.1;
DR PIR: S47023; S47023.
DR PROSITE: PS00446; RNA_POL.D 30KD; 1.
KW Transiferase; DNA-directed RNA polymerase; Transcription.
SQ SEQUENCE 264 AA; 29612 MW; C5B491B CRC32;

Query Match 30.7%; Score 62; DB 1; Length 264;
Best Local Similarity 47.4%; Pred. No. 6 40e-01;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Db 170 VTGNCERAVECPGAYF 188
OY 2 vphlgdrektrdsvcpqky 20

RESULT 9
ID SECA-TREPA STANDARD; PRT; 916 AA.
AC O83394;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE PREPROTEIN TRANSLOCASE SECA SUBUNIT.
GN SECA OR TP0379.
OS Treponema pallidum.
CC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NICHOES;
RX MEDLINE: 98332770.
RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
RA DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
RA KNOXBERG E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
RA KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
RA MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
RA HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
RA VENTER J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete".
RL Science 281:375-388(1998).
CC -1- FUNCTION: INVOLVED IN PROTEIN EXPORT. INTERACTS WITH THE SECY/SECE
CC SUBUNITS. SECA HAS A CENTRAL ROLE IN COUPLING THE HYDROLYSIS OF
CC ATP TO THE TRANSFER OF PRE-SECRETORY PERIPLASMIC AND OUTER
CC MEMBRANE PROTEINS ACROSS THE MEMBRANE (BY SIMILARITY).
CC -1- SUBUNIT: PART OF THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS
CC WHICH COMPRISE SECA, SECB, SECD, SECE, SECF, SECG AND SECH
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF PLASMA MEMBRANE
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SECA FAMILY.
CC -----
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CC -----
DR EMBL: AE001217; AAC65365.1;
DR TIGR: TP0379;
DR PFAM: PF01043; SecA_protein; 1.
KW Protein transport; ATP-binding; Membrane; Translocation; Transport.
FT NP-BIND 103 110 ATP (POTENTIAL).
SQ SEQUENCE 916 AA; 103779 MW; 84D5AFAC CRC32;

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CC -----
DR EMBL: Z95620; CAB09117.1; -.
RW PFAM: PF01423; Sm; 1.
KW Hypothetical protein; Nuclear protein; Ribonucleoprotein.
SQ SEQUENCE 140 AA; 16171 MW; 4092112C CRC32;
-----
Query Match 29.2%; Score 59; DB 1; Length 140;
Best Local Similarity 31.8%; Pred. No. 2.65e+00;
Matches 7; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
-----
DB 106 LAKHEERKNRKNRKYLS 127
OY 2 vphlgdrkridsvcpqgkylnp 23
-----
RESULT 13
ID INT6_MOUSE STANDARD; PRT; 445 AA.
AC Q64252; Q64058; Q64059;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VIRAL INTEGRATION SITE PROTEIN INT-6.
GN INT6 OR INT-6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RS SEQUENCE FROM N.A.
RX MEDLINE: 95156630.
RA MARCHETTI A., BUTTIGTA F., MIRAZAKI S., GALLAHAN D., SMITH G.H.,
RA CALLAHAN R.;
RT "Int-6, a highly conserved, widely expressed gene, is mutated by
RT mouse mammary tumor virus in mammary preneoplasia.";
RT J. Virol. 69:1932-1938(1995).
RN [2]
RS SEQUENCE FROM N.A.
RX MEDLINE: 97405883.
RA DIELLA F., LEVI G., CALLAHAN R.;
RT "Characterization of the INT6 mammary tumor gene product.";
RT DNA Cell Biol. 16:839-847(1997).
RN [3]
RS REVISIONS TO N-TERMINUS.
RA CALLAHAN R.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION BEGINS AT DAY 8 OF EMBRYONIC
CC DEVELOPMENT.
CC -1- DISEASE: INT-6 SERVES AS A SITE FOR VIRAL INTEGRATION OF MOUSE
CC MAMMARY TUMOR VIRUS (MMTV) IN MAMMARY TUMORS.
CC -----
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CC -----
DR EMBL: L35556; AB97930.1; -.
DR EMBL: S75221; AAC00046.1; -.
DR EMBL: S75223; AAC00047.1; -.
DR MGI: 99257; INT6.
DR PFAM: PF01399; PCI; 1.
KW Proto-oncogene.
FT VARIANT 158 158 V -> N (IN MMTV-INDUCED TUMOR 1139-1).
FT VARIANT 159 445 MISSING (IN MMTV-INDUCED TUMOR 1139-1).
FT VARIANT 158 180 VPATRNALSLSLMGKLAELIMQ -> LPQSDLAETATVC

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FT FT GTTLKAVMDR (IN MATV-INDUCED TUMOR  

FT FT 1139-2).  

FT FT VLVNDFEVLALDEPIENARLFIETPRRIQCSINMLA  

FT FT DLKNMTE -> LNIKEFOSKGIRIVQAASGWEIIRA  

FT FT AVGRPEHGRIGDPLENG (IN MATV-INDUCED  

FT FT TUMOR 22).  

FT FT MISSING (IN MATV-INDUCED TUMOR 22).  

FO SEQUENCE 445 AA; 52220 MW; E7ZICJ39 CRC32;  

DB 66 IPH-ALEKRITVAQLKOLAEETPT 91  

Oy :||| ||| |::|:  

2 vphlgdrkrdvcpqgkylnpqxns1 28  

RESULT 14  

ID PSS1_HUMAN STANDARD; PRT; 473 AA.  

AC P46651;  

DT 01-FEB-1996 (Rel. 33, Created)  

DT 01-FEB-1996 (Rel. 33, Last sequence update)  

DI 01-NOV-1997 (Rel. 35, Last annotation update)  

DE PHOSPHATIDYLSERINE SYNTHASE I (SERINE-EXCHANGE ENZYME I) (EC 2.7.8.-)  

DN (KIAA0024).  

GN PSSA.  

OS Homo sapiens (Human).  

OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;  

OC Eutheria; Primates; Catarrhini; Homidae; Homo.  

RN [1]  

RP SEQUENCE FROM N.A.  

RC TISSUE-BONE MARROW;  

RX MEDLINE; 96051387.  

RA NOMURA N., MIYAJIMA N., SAZUKA T., TANAKA A., KAWABAYASHI Y.,  

RA SANO S., NAGASE T., SEKI N., ISHIWATA K.-I., TABARA S.;  

RT "Prediction of the coding sequences of unidentified human genes. I.  

RT The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by  

RT analysis of randomly sampled cDNA clones from human immature myeloid  

RT cell line KG-1.";  

RL DNA Res. 1:27-35(1994).  

CC -I- FUNCTION: BASE-EXCHANGE REACTION BETWEEN FREE L-SERINE AND THE  

CC POLAR HEAD GROUPS OF PRE-EXISTING PHOSPHOLIPIDS. IT CAN UTILIZE  

CC PHOSPHATIDYLCHOLINE AS A PHOSPHATIDYL DONOR. IT CAN ALSO CATALYZES  

CC THE CHOLINE AND ETHANOLAMINE BASE-EXCHANGE REACTIONS.  

CC -I- PATHWAY: COMMITTED STEP IN THE SYNTHESIS OF PHOSPHATIDYLSERINE.  

CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  

CC -----  

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CC -----  

CC EMBL; D14694; BAA03520.1;  

KW Transference; Phospholipid biosynthesis; Transmembrane.  

DR TRANSMEM 36 56 POTENTIAL.  

FT TRANSMEM 73 93 POTENTIAL.  

FT TRANSMEM 103 123 POTENTIAL.  

FT TRANSMEM 161 181 POTENTIAL.  

FT TRANSMEM 187 207 POTENTIAL.  

FT TRANSMEM 217 237 POTENTIAL.  

FT TRANSMEM 287 307 POTENTIAL.  

FT TRANSMEM 310 330 POTENTIAL.  

FT TRANSMEM 356 376 POTENTIAL.  

FT TRANSMEM 384 404 POTENTIAL.  

SQ SEQUENCE 473 AA; 55527 MW; D81f6EF2 CRC32;  

Query Match 29.2%; Score 59; DB 1; Length 445;  

Best Local Similarity 37.0%; Pred. No. 2,65e+00;  

Matches 10; Conservative 10; Mismatches 6; Indels 1; Gaps 1;  


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Page 8

Wed Apr 19 10:35:35 2000

DB 408 HYGHEKTSCECDGT 424
 QY 4 hlgdrekdrsvcpqgky 20

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RESULT 15
ID 66PL CLAMI STANDARD; PRT; 568 AA.
AC P54237;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC 1 (GPI) (EC 5.3.1.9)
DE (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHT).
GN PGIC1
OS Clarkia miltrediae;
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosid II; Myrtales; Onagraceae; Clarkia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-POPULATION WEEDEN 165A;
RA GOTTLEIB L.D., FORD V.S.;
RT "Phylogenetic relationships among the sections of Clarkia (Onagraceae)
RT inferred from the nucleotide sequences of PgiC."
RL Syst. Bot. 21:1-18(1996)
CC -1- CATALYTIC ACTIVITY: GLUCOSE 6-PHOSPHATE - FRUCTOSE 6-PHOSPHATE.
CC -1- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE GPI FAMILY.
CC -----
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CC -----
CC EMBL: X89389; CAA61569.1; -.
CC DR PROSITE: PS00765; P_GLUCOSE_ISOMERASE_1; 1.
CC DR PROSITE: PS00174; P_GLUCOSE_ISOMERASE_2; 1.
CC DR PRAM: PF00342; PGI; 1.
CC KW Glucneogenesis; Glycolysis; Isomerase; Multigene family.
CC SQ SEQUENCE 568 AA; 62664 MW; 703D6218 CRC32;

Query Match 29.2%; Score 59; DB 1; Length 568;
Best Local Similarity 41.7%; Pred. No. 2.65e+00;
Matches 10; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

DB 95 VLHVALRAPRDSAICSDGNVPPD 118
QY 2 vphlgdrekdrsvcpqgkylnhpq 24
  
```

Search completed: Tue Apr 18 11:07:36 2000
 Job time : 31 secs.

 W P E R E H (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 18 11:07:54 2000; Maspar time 66.86 Seconds

Tabular output not generated.

Title: >PEP1.PEP
 Description: (1-28) from new pep
 Perfect Score: 202
 Sequence: 1 lvphlgdrekrdsvcpqgkylnhpqnsi 28

Scoring table: PAM 150
 Gap 15

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 08
 Listing first 45 summaries

Database:

sptrembl12
 1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
 13:sp_vertebrate 14:sp_virus

Statistics: Mean 28.745; Variance 34.322; scale 0.837

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	167	82.7	189	6	Q95185	TUMOUR NECROSIS FACTOR	4.85e-29
2	149	73.8	471	6	Q19131	TUMOR NECROSIS FACTOR-	1.26e-23
3	145	71.8	189	6	Q97530	TUMOR NECROSIS FACTOR	1.93e-22
4	74	36.6	213	2	Q32029	YRRT PROTEIN.	2.98e-03
5	69	34.2	132	11	Q35324	EMS/FIL1 ACTIVATED TRA	4.07e-02
6	68	33.7	483	3	Q94206	OXIDOREDUCTASE.	6.77e-02
7	66	32.7	467	5	Q15993	PJCHI-3.	1.85e-01
8	66	32.2	687	5	Q23729	THROMBOSPONDIN RELATED	3.04e-01
9	65	32.2	1376	5	Q26637	5 ALPHA FIBRILLAR COLL	3.04e-01
10	65	32.2	1728	5	Q25425	P-GLYCOPROTEIN.	3.04e-01
11	63	31.2	506	10	Q65727	SQUALENE EPOXIDASE HOM	8.05e-01
12	63	31.2	518	10	Q65726	SQUALENE EPOXIDASE HOM	8.05e-01
13	63	31.2	563	14	Q82794	L PROTEIN.	8.05e-01
14	62	30.7	307	10	Q9X111	F7H1.9 PROTEIN.	1.30e+00
15	62	30.7	414	5	Q25308	SQUALENE SYNTHASE.	1.30e+00
16	62	30.7	563	2	Q52200	ACTIVATOR.	1.30e+00
17	62	30.7	699	1	Q9YF81	699AA LONG HYPOHETICA	1.30e+00
18	62	30.7	774	3	Q42918	POTATIVE ALPHA-NAYLASE	1.30e+00
19	62	30.7	1187	2	Q59278	ENDOXYLANASE (EC 3.2.1	1.30e+00
20	62	30.7	2664	5	Q26033	VARIANT-SPECIFIC SUPRA	1.30e+00

21	61	30.2	313	3	Q94524	CONSERVED HYPOTHETICAL	2.09e+00
22	61	30.2	336	10	Q92FW3	T30D6.19 PROTEIN.	2.09e+00
23	61	30.2	563	2	Q52177	PHR GENE.	2.09e+00
24	61	30.2	837	4	Q75173	KIAA0688 PROTEIN.	2.09e+00
25	61	30.2	850	2	Q92656	MAINOPEPTIDASE N.	2.09e+00
26	61	30.2	3623	11	Q70244	INTRINSIC FACTOR-B12 R	2.09e+00
27	60	29.7	88	2	Q86354	RSR2.	3.34e+00
28	60	29.7	89	3	P79072	HYDROPHOBIN.	3.34e+00
29	60	29.7	313	1	Q29863	CONSERVED HYPOTHETICAL	3.34e+00
30	60	29.7	696	14	P88947	ORF K10.	3.34e+00
31	60	29.7	696	14	Q40939	ORF K10.	3.34e+00
32	60	29.7	928	4	Q9Y2L1	KIAA1008 PROTEIN.	3.34e+00
33	60	29.7	3034	11	Q35161	SEVEN-PASS TRANSMEMBR	3.34e+00
34	60	29.7	3432	14	Q92928	POLYPROTEIN PRECURSOR.	3.34e+00
35	59	29.2	245	4	Q15112	CARBOXY-PROPEPTIDE OF	5.30e+00
36	59	29.2	406	10	Q43509	G-BOX BINDING PROTEIN	5.30e+00
37	59	29.2	431	4	Q94800	HRHFE2060 PROTEIN (FR	5.30e+00
38	59	29.2	445	4	Q43902	EUKARYOTIC TRANSLATION	5.30e+00
39	59	29.2	473	11	Q55024	PHOSPHATIDYL SERINE SYN	5.30e+00
40	59	29.2	564	11	Q70604	COLLAGEN ALPHA 1 (III)	5.30e+00
41	59	29.2	614	5	Q15702	REDA (FRAGMENT).	5.30e+00
42	59	29.2	1544	4	Q9Y305	PLU-1 PROTEIN.	5.30e+00
43	59	29.2	1580	4	Q95811	RETINOBLASTOMA BINDING	5.30e+00
44	58	28.7	769	2	Q68843	GLYCOSIDASE OLER.	8.37e+00
45	58	28.7	3432	14	Q9WCX7	POLYPROTEIN.	8.37e+00

ALIGNMENTS

RESULT ID	1	PRELIMINARY	PRT	189 AA.
AC Q95185				
DT 01-FEB-1997 (TREMBlrel. 02, Created)				
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)				
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)				
DE TUMOUR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).				
GN TNFR-1.				
OS Felis silvestris catus (Cat).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.				
RN [1]				
RP SEQUENCE FROM N.A.				
RU DUTHE S., NASIR L., ECKERSALL P.D.;				
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.				
DR EMBL: U72344; AAB95089.1; ..				
DR HSP: P19438; IEXT.				
DR PROSITE: PS00652; TNFR_NGFR_1; 3.				
DR PFAM: PF00020; TNFR_C6; 3.				
FT NON TER 189				
DR				
SO SEQUENCE 189 AA; 21420 MW; 687732D2 CRC32;				

Query Match 82.74; Score 167; DB 6; Length 189;
 Best Local Similarity 82.18; Pred. No. 4.85e-29;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DB 30 LVPHLGRDREKRAIPCPQGYHHPDINSI 57	
QY 1 LVPHLGRDREKRDVCPQGYHHPQNSI 28	
RESULT 2	
AC Q19131; PRELIMINARY; PRT; 471 AA.	
DT 01-JAN-1998 (TREMBlrel. 05, Created)	
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)	
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)	
DE TUMOUR NECROSIS FACTOR-RECEPTOR I.	
GN TNF-R1.	
OS Bos taurus (Bovine).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;	
OC Bovinae; Bos.	
RN [1]	

RP SEQUENCE FROM N.A.
 RC TISSUE-AORTA;
 RA LEE E.-K., TALYOR M.J., KERRELL M.E.;
 RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U90937; AAB65143.1; -
 DR HSSP: P19438; 1TNR.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PFAM; PF00531; death; 1.
 DR PFAM; PF00020; TNFR_C6; 3.
 DR SEQUENCE 471 AA; 51367 MW; 1D60FPA4 CRC32;
 SO
 Query Match 73.8%; Score 149; DB 6; Length 471;
 Best Local Similarity 71.4%; Pred. No. 1.26e-23;
 Matches 20; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 DB 30 LYPHGDLEKRESPOGKRYNHPQNSTI 57
 1 LYPHGDLEKREKIDSVCPGQKYLHPQXNSI 28
 ID 097530 PRELIMINARY; PRT; 189 AA.
 AC 097530;
 DT 01-MAY-1999 (TRENBLrel. 10; Created)
 DT 01-MAY-1999 (TRENBLrel. 10; Last sequence update)
 DT 01-NOV-1999 (TRENBLrel. 12; Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA DUTHIE S., NASIR L., ARGYLE D.J., ECKERSALL P.D.;
 RL "Canine tumor necrosis factor receptor, partial cds."
 DR EMBL; AF013955; AAD01516.1; -
 DR HSSP; P19438; 1TNR.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR Receptor.
 KW NON_TER
 FT NON_TER 189
 SO SEQUENCE 189 AA; 21324 MW; 2A93BEF CRC32;
 Query Match 71.8%; Score 145; DB 6; Length 189;
 Best Local Similarity 67.9%; Pred. No. 1.93e-22;
 Matches 19; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 DB 30 LYPHPRNRKRAILCPQGRYHPQDDSI 57
 1 LYPHGDLEKREKIDSVCPGQKYLHPQXNSI 28
 QY
 RESULT 4
 ID 032029 PRELIMINARY; PRT; 213 AA.
 AC 032029;
 DT 01-JAN-1998 (TRENBLrel. 05; Created)
 DT 01-JAN-1998 (TRENBLrel. 05; Last sequence update)
 DT 01-NOV-1998 (TRENBLrel. 06; Last annotation update)
 DE YRRT PROTEIN.
 GN Bacillus subtilis.
 OS Bacteria; Firmicutes; Bacillus/Clostridium group;
 CC Bacillus/Staphylococcus group; Bacillus.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RA MEDLINE; 98044033.
 RA KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
 RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
 RA BORRIS R., BOURSIER L., BRANS A., BRAUN M., BRIGHELL S.C., BRON S.,
 RA BROUILLET S., BRUSCHI C.V., CALDWELL B., CAVANO V., CARTER N.M.,
 RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
 RA DENIZOT F., DEVINE K.M., DOSTERHOF A., EHRLICH S.D., EMMERSON P.T.,

RA ENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOULGER D.,
 RA FRITZ C., FUJITA M., FUJITA Y., FUMA S., GALIZZI A., GALLERON N.,
 RA GRIM S.Y., GLASER P., GOFFEAU A., GOLIGITLY E.J., GRANDI G.,
 RA GUISEPI G., GUY B.J., HAGA K., HAIBCH J., HARWOOD C.R., HENAUT A.,
 RA HUBERT H., HOLAPPEL S., HOSONO Y., HULLO M.F., ITAYA M., JONES L.,
 RA JORIS B., KARAMATA D., KASHARA Y., KLAER-BLANCHARD M., KLEIN C.,
 RA KOBAYASHI Y., KOETTER P., KONIGSTEIN G., KROGH S., KUMANO M.,
 RA KURITA K., LAPIDUS A., LARDINOIS S., LABER J., LAZAREVIC V.,
 RA LEE S.M., LEVINE A., LIU H., MASUDA S., MAEL C., MEDIGUE C.,
 RA MEDINA N., MELIENDO R.F., MIZUNO M., MOESTL D., NAKAI S., NOBACK M.,
 RA NOONE D., O'REILLY M., OGAWA K., OGIMARA A., ODEGA B., PARK S.H.,
 RA PARRO V., POHL T.M., PORTELELL D., PORROLIK S., PRESCOTT A.M.,
 RA PRESECAN E., PUIC P., PURTELLE B., RAPPORT G., REY M., REYNOLDS S.,
 RA RIGER M., RIVOLTA C., ROCHA E., ROCHE B., ROSE M., SADATE Y.,
 RA SATO T., SCANLAN E., SCHLEICH S., SCHROETER R., SCOPONE F.,
 RA SERIGUCHI J., SEKONKA A., SEROK S.J., SERROR P., SHIN B.S., SOLDO B.,
 RA SOROKIN A., TACCONI E., TAKAGI T., TAKAHASHI H., TAKEKAWA K.,
 RA TAKEUCHI M., TAMAKOSHI A., TANAKA T., TERPSTRA P., TIGNONI A.,
 RA TOSATO V., UCHIYAMA S., VANDENBOL M., VANIER F., VASSAROTI A.,
 RA VIARI A., MAMBUUT R., WEDLER E., WEDLER H., WEITZNEGER T.,
 RA WINTERS P., WIPAT A., YAMAMOTO H., YAMANE K., YASUNO K., YATA K.,
 RA YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E., YOSHIKAWA H., DANCHIN A.,
 RA "The complete genome sequence of the gram-positive bacterium Bacillus
 subtilis."
 RL Nature 390:249-256(1997).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RA KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
 RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL; 299117; CAB14670.1; -
 DR PFAM; PF00398; Rnrad; 1.
 DR SEQUENCE 213 AA; 24196 MW; ED4EFC11 CRC32;
 SO
 Query Match 36.6%; Score 74; DB 2; Length 213;
 Best Local Similarity 40.0%; Pred. No. 2.98e-03;
 Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
 DB 119 HLTDEKRAIKQYGGKYLHDKIV 143
 4 HLTDEKREKIDSVCPGQKYLHPQXNSI 28
 QY
 RESULT 5
 ID 035324 PRELIMINARY; PRT; 132 AA.
 AC 035324;
 DT 01-JAN-1998 (TRENBLrel. 05; Created)
 DT 01-JAN-1998 (TRENBLrel. 05; Last sequence update)
 DT 01-NOV-1998 (TRENBLrel. 12; Last annotation update)
 DE EMS/FLII ACTIVATED TRANSCRIPT 2.
 GN EAT-2.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC MEDLINE; 97152556.
 RA THOMPSON A.D., BRAUN B.S., ARYAND A., STEWART S.D., MAY W.A., CHEN E.,
 RA KORENBERG J., DENNY C.;
 RA "EAT-2 is a novel SH2 domain containing protein that is up regulated
 RT by Ewing's sarcoma EMS/FLII fusion gene."
 RL Oncogene 13:2649-2658(1996).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC THOMPSON A.D., BRAUN B.S., ARYAND A., STEWART S.D., MAY W.A., CHEN E.,
 RA KORENBERG J., DENNY C.;
 RA Submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF020263; AAB70923.1; -
 DR HSSP; P12931; 1SHD.
 DR PFAM; PF00017; SH2; 1.
 DR SEQUENCE 132 AA; 15258 MW; 3126FD44 CRC32;
 SO
 Query Match 34.2%; Score 69; DB 11; Length 132;

Best Local Similarity 36.8%; Pred. No. 4,07e-02;
Matches 7; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

DB 93 LVVHLSNPINNNICORGR 111

OY 1 lvphlgdrekrdsvcpqgk 19

RESULT 6
ID 094206 PRELIMINARY; PRT; 483 AA.
AC 094206;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE OXIDOREDUCTASE.
GN OX1.
OS Claviceps purpurea (ergot fungus).
OC Eukaryota; Fungi; Ascomycota; Euascomycetes; Pyrenomycetes;
OC Hypocreales; Clavicipitaceae; Claviceps.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-P1;
RX MEDLINE: 99168777.
RA TUDKINSKI P., HOELTER K., CORREIA T.H., ARNTZ C., GRAMMEL N.,
RA KELLER U.;
RT "Evidence for an ergot alkaloid gene cluster in Claviceps purpurea."
RL Mol. Genet. 261:133-141(1999).
DR EMBL: AJ011965; CAB39328.1; -
SQ SEQUENCE 483 AA; 52025 MW; 9A9D6210 CRC32;

Query Match 33.7%; Score 68; DB 3; Length 483;
Best Local Similarity 63.6%; Pred. No. 6,77e-02;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

DB 2 ERKQSTCPOGR 12

OY 9 ekrdsvcpqgk 19

RESULT 7
ID 015993 PRELIMINARY; PRT; 467 AA.
AC 015993;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DE 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE PICH-3.
OS Pennaeus japonicus (Kuruma prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeidae;
OC Pennaeus.
RN [1]
RP SEQUENCE FROM N.A.
RA WATANABE T., KONO M., AIDA K., NAGASAWA H.;
RL Blochim. Biophys. Acta 0:0-0(1997).
DR EMBL: AB008027; BAA22854.1; -
DR HSSP: P07254; ICTN.
DR PRAM: PF01607; Chitin_bind_2; 1.
DR PRAM: PF00704; Glyco_hydro_18; 1.
SQ SEQUENCE 467 AA; 51765 MW; 5AF8F811 CRC32;

Query Match 32.7%; Score 66; DB 5; Length 467;
Best Local Similarity 36.8%; Pred. No. 1,85e-01;
Matches 7; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

DB 427 GGFDEKEEVCPEGTLPNQ 445

OY 6 gdrkrdsvcpqgkylnpq 24

RESULT 8
ID 023729 PRELIMINARY; PRT; 687 AA.
AC 023729;
DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE THROMBOSPONDIN RELATED ADHESIVE PROTEIN (TRAP-C1).
GN TRAP-C1.
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MOREDUN;
RX MEDLINE: 98234217.
RA SPANO F., PUTIGNANI L., NAITZA S., PURI C., WRIGHT S., CRISANTI A.;
RT "Molecular cloning and expression analysis of a Cryptosporidium parvum
gene encoding a new member of the thrombospondin family."
RL Mol. Biochem. Parasitol. 92:147-162(1998).
RN [2]

RP SEQUENCE OF 300-491 FROM N.A.
RC STRAIN-M1 ISS-1;
RA SPANO F.S., RANDUCCI L.R., CATTERUCCIA F.C., SACCHIO S.S.,
RA CRISANTI A.C.;
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF017267; AAC48311.1; -
DR EMBL: X77587; CA54690.1; -
DR PRAM: PF00090; tsp_1; 5.
SQ SEQUENCE 687 AA; 75985 MW; B681E28C CRC32;

Query Match 32.2%; Score 65; DB 5; Length 687;
Best Local Similarity 36.4%; Pred. No. 3,04e-01;
Matches 8; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

DB 299 GKNKTRDADCPTGCIHNEWSS 320

OY 6 gdrkrdsvcpqgkylnpqxn 27

RESULT 9
ID 026637 PRELIMINARY; PRT; 1376 AA.
AC 026637;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE 5 ALPHA FIBRILLAR COLLAGEN (FRAGMENT).
GN COL5ALPHA.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidae;
OC Euechinozoa; Echinozoa; Echinoidae; Strongylocentrotidae;
OC Strongylocentrotus.
RN [1]
RP SEQUENCE FROM N.A.
RA EXPOSITO J.V., BOUVE N., DELAGE G., GARRONE R.;
RT "Characterization of two genes coding for a similar four-cysteine
motif of the amino-terminal propeptide of a sea urchin fibrillar
RT collagen."
RL Eur. J. Biochem. 234:59-65(1995).
DR EMBL: X89800; CAA61928.1; -
DR EMBL: X89801; CAA61928.1; JOINED.
DR EMBL: X89802; CAA61928.1; JOINED.
DR EMBL: X89803; CAA61928.1; JOINED.
DR EMBL: X89804; CAA61928.1; JOINED.
DR EMBL: X89805; CAA61928.1; JOINED.
DR HSSP: P80546; ITOI.
DR PRAM: PF00093; yvc; 1.
DR PRAM: PF00093; yvc; 1.
FT NON_TER
SQ SEQUENCE 1376 AA; 151182 MW; A1126C57 CRC32;

Query Match 32.2%; Score 65; DB 5; Length 1376;
Best Local Similarity 38.5%; Pred. No. 3,04e-01;
Matches 10; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

DB 890 FVPLVTNEDMTDKPCQVYKICNEVN 915

OY 1 lvphlgdrekrdsvcpqgkylnpqxn 26

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RESULT 10
ID Q25425; PRELIMINARY; PRT; 1724 AA.
AC Q25425;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE P-GLYCOPROTEIN.
OS Leishmania tarentolae (Sauriella leishmania tarentolae).
OC Eukaryota; Eukaryota; Kinetoplastida; Trypanosomatidae; Leishmania.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TARI;
RX MEDLINE; 95198776.
RA LEGARE D., HETTEMER E., OUELLETTE M.;
RT "The P-glycoprotein-related gene family in Leishmania.";
RL MCL. Biochem. Parasitol. 68:81-91(1994).
DR EMBL; L29485; AAA5541.1; -.
DR HSP; P13869; INED.
DR PFAM; PF00664; ABC_membrane; 2.
DR PFAM; PF00005; ABC_tran; 2.
SQ SEQUENCE 1724 AA; 188967 MW; C9F31C24 CRC32;

Query Match 32.28; Score 65; DB 5; Length 1724;
Best Local Similarity 40.0%; Pred. No. 3.04e-01;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

DB 913 LDAHGERVMBRCIC 927
QY 1 LVPHLGRKIDSV 15

RESULT 11
ID Q65727; PRELIMINARY; PRT; 506 AA.
AC Q65727;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE SQUALENE EPOXIDASE HOMOLOGUE (EC 1.14.99.7) (SQUALENE MONOOXYGENASE).
GN SGP1.1.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Brassica.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. WESTAR; TISSUE-SHOOTS;
RA SCHAFER U.A., REED D.W., HUNTER D.G., YAO K., WENINGER A.M.,
RA TSANG E.W.T., REANEY M.J.T., MACKENZIE S.L., COVELLO P.S.;
RL Submitted (May-1998) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: SQUALENE + AH(2) + O(2) -> (S)-SQUALENE-2,3-
CC EPOXIDE + A + H(2)O.
CC -1- CORFACTOR: FAD.
DR EMBL; AJ005931; CA06773.1; -.
DR MENDEL; 29854; Brana.3399;29854.
KW Oxidoreductase.
SQ SEQUENCE 506 AA; 55571 MW; 04226965 CRC32;

Query Match 31.28; Score 63; DB 10; Length 506;
Best Local Similarity 30.0%; Pred. No. 8.05e-01;
Matches 6; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

DB 74 HYTERDMREPVMMGEFMP 93
QY 4 HLGDKRIDSVCPGKYHP 23

RESULT 12
ID Q65726; PRELIMINARY; PRT; 518 AA.
AC Q65726;
DT 01-AUG-1998 (TREMBlrel. 07, Created)

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DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE SQUALENE EPOXIDASE HOMOLOGUE (EC 1.14.99.7).
GN SGP1.2.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Brassica.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. WESTAR; TISSUE-SHOOTS;
RA SCHAFER U.A., REED D.W., HUNTER D.G., YAO K., WENINGER A.M.,
RA TSANG E.W.T., REANEY M.J.T., MACKENZIE S.L., COVELLO P.S.;
RL Submitted (May-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ005928; CA06770.1; -.
DR MENDEL; 29850; Brana.3399;29850.
KW Oxidoreductase.
SQ SEQUENCE 518 AA; 57400 MW; 5F28687E CRC32;

Query Match 31.28; Score 63; DB 10; Length 518;
Best Local Similarity 30.0%; Pred. No. 8.05e-01;
Matches 6; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

DB 75 HYTERDMREPVMMGEFMP 94
QY 4 HLGDKRIDSVCPGKYHP 23

RESULT 13
ID Q82794; PRELIMINARY; PRT; 563 AA.
AC Q82794;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE L PROTEIN.
GN MBGGENE.
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/PPV/DUTCH/27 (H7N7), DUTCH;
RA MUNK K., PRITZER E., KRETZSCHMAR E., GUTTE B., GARTEN W., KLENK H.;
RL Glycobiology 0:0-0(1992).
DR EMBL; Z12617; CA078263.1; -.
DR PFAM; PF00509; Hemagglutinin; 1.
DR PRINTS; PR00329; HEMAGGLUTININ2.
DR PRINTS; PR00330; HEMAGGLUTININ1.
DR PRINTS; PR00331; HEMAGGLUTININ2.
SQ SEQUENCE 563 AA; 62883 MW; 6D36FAC1 CRC32;

Query Match 31.28; Score 63; DB 14; Length 563;
Best Local Similarity 33.38; Pred. No. 8.05e-01;
Matches 6; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

DB 97 ERRERNDVCYPGKFNVE 114
QY 7 DREKIDSVCPGKYHPQ 24

RESULT 14
ID Q9X111; PRELIMINARY; PRT; 307 AA.
AC Q9X111;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE F7H1.9 PROTEIN.
GN F7H1.9.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;

```


OC Arabidopsis.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA LIN X., KAUT S., SHEA T.P., FUJII C.Y., SHEN M., VANAKEN S.E.,
 RA BARNSTEAD M.E., MASON T.M., BOWMAN C.L., RONNING C.M., BENITO M.,
 RA CARRERA A.J., CREASY T.H., BUELL C.R., TOWN C.D., NIERMAN W.C.,
 RA FRASER C.M., VENTER J.C.;
 RT "Arabidopsis thaliana chromosome II BAC F7H1 genomic sequence.";
 RL Submitted (Jul-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC007134; AAD26930.1; -;
 SQ SEQUENCE 307 AA; 33640 MM; 079BE7E6 CRC32;

Query Match 30.7%; Score 62; DB 10; Length 307;
 Best Local Similarity 50.0%; Pred. No. 1.30e+00;
 Matches 10; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

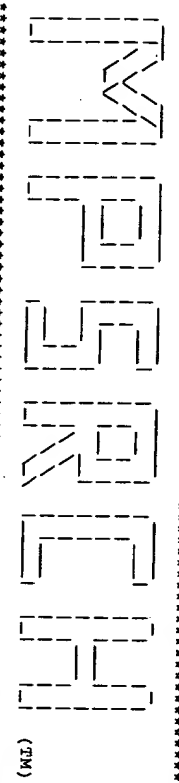
DB 253 LPHRATRGKRPNCPPGR 272
 QY 1 lvphlgdrekrdsv-cpqrk 19

RESULT 15
 ID 025308 PRELIMINARY; PRT; 414 AA.
 AC 025308;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE SQUALENE SYNTHASE.
 OS Leishmania major.
 OC Eukaryota; Euzoenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRIEDLIN VI;
 RA COFRIM P.C., GARITY L., BEVERLEY S.M.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U30455; AAC17923.1; -;
 DR PFM; PR00494; SOS_PSY.1.
 SQ SEQUENCE 414 AA; 46844 MM; FB8AA048 CRC32;

Query Match 30.7%; Score 62; DB 5; Length 414;
 Best Local Similarity 40.0%; Pred. No. 1.30e+00;
 Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

DB 48 VVAQLADQQLDAIC 62
 QY 1 lvphlgdrekrdsv-c 15

Search completed: Tue Apr 18 11:09:07 2000
 Job time : 73 secs.



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Mpsrch.p protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Apr 18 11:05:10 2000; Maspar time 24.88 Seconds
26.654 Million cell updates/sec
Tabular output not generated.

Title: >PEP1.PEP
Description: (1-28) from new.pep
Perfect Score: 202
Sequence: 1 lvpnlgtrekrdsvcpgkyihpqnsl 28

Scoring table: PAM 150
Gap 15

Searched: 188963 segs, 23666106 residues
Post-processing: Minimum Match 0%

Database: a:geneseq36
1:geneseqp

Statistics: Mean 21.488; Variance 63.322; scale 0.339

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description	Pred. No.
1	202	100.0	28	1 R1072	Peptide fragment #1 of	1.00e-16
2	202	100.0	102	1 R10984	Partial sequence 30kd	1.00e-16
3	202	100.0	154	1 R24082	Truncated TNF-alpha 55	1.00e-16
4	202	100.0	159	1 R24083	Truncated TNF-alpha 55	1.00e-16
5	202	100.0	158	1 R24084	Truncated TNF-alpha 55	1.00e-16
6	202	100.0	159	1 R24080	Truncated TNF-alpha 55	1.00e-16
7	202	100.0	211	1 W89225	Tumour necrosis factor	1.00e-16
8	202	100.0	309	1 R70108	Tumour necrosis factor	1.00e-16
9	202	100.0	311	1 W89228	Tumour necrosis factor	1.00e-16
10	202	100.0	366	1 W89228	Tumour necrosis factor	1.00e-16
11	202	100.0	371	1 R07449	Tumour necrosis factor	1.00e-16
12	202	100.0	397	1 W89227	Tumour necrosis factor	1.00e-16
13	202	100.0	417	1 W89226	Tumour necrosis factor	1.00e-16
14	202	100.0	420	1 W89226	Tumour necrosis factor	1.00e-16
15	202	100.0	433	1 R51032	Mutant p55 tumour necr	1.00e-16
16	202	100.0	443	1 R51033	Mutant p55 tumour necr	1.00e-16
17	202	100.0	451	1 R70107	TNF-R-GPB 130 fusion p	1.00e-16
18	202	100.0	455	1 R12550	Type I TNF receptor.	1.00e-16
19	202	100.0	455	1 R42059	Lambda derived TNF-R.	1.00e-16
20	202	100.0	455	1 R42197	p55 tumour necrosis fa	1.00e-16
21	202	100.0	455	1 R51034	Mutant p55 tumour necr	1.00e-16
22	202	100.0	455	1 R75084	p55 TNF-R.	1.00e-16
23	202	100.0	455	1 R07451	Human Tumour Necrosis	1.00e-16

ALIGNMENTS

RESULT ID	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
AC	R1072	standard;	peptide;	28	AA.																			
DE	24-MAY-1991	(first entry)																						
DT	Peptide fragment #1 of 55kd	TNF-binding protein.																						
DE	Tumour Necrosis Factor;	binding proteins; septic shock;																						
KW	autoimmune glomerulonephritis;	lymphokine; cytokine.																						
FN	EP-417563-A.																							
PD	20-MAR-1991.																							
PF	31-AUG-1990;	116707.																						
PR	12-SEP-1989;	CH-003319.																						
PR	08-MAR-1990;	CH-000746.																						
PR	20-APR-1990;	CH-001347.																						
PA	(HOFF) HOFFMANN-LA ROCHE AG.																							
PI	Brockhaus M; Dembic Z, Gentz R, Lesslauer W, Lotscher H;																							
PI	Schlaeger EJ;																							
DR	WPI; 91-081851/12.																							
PT	Insoluble tumour necrosis factor binding proteins - and DNA																							
PT	encoding them, useful in pharmaceutical prods. and for antibody																							
PT	prodn.																							
CS	Claim 3; Page 19; 26pp; German.																							
CC	Cells which produce TNF-binding proteins (-BP)(eg HL60 cells) were																							
CC	cultured and the supernatant centrifuged, put on a column of																							
CC	"Affigel 10" to which recombinant TNF-alpha was bonded, and TNF-BP																							
CC	eluted. The recovered protein was used as an immunogen to raise																							
CC	monoclonal antibodies. The MAbs were attached to Sepharose 4B and																							
CC	cell extract purified on a system of: BSA-Sepharose 4B; Ab-Sepharose-																							
CC	4B and TNF alpha-Sepharose 4B. Active TNF-BP were eluted from the																							
CC	last two columns and separated by gel electrophoresis to identify																							
CC	bands of mol. wt. 875, 65, 55, 51, 38, 36 and 34kd. Partial amino																							
CC	acid sequences were determined for the 75 and 55kd proteins,																							
CC	including the fragment given here which is a minimum sequence for																							
CC	TNF-binding.																							
CC	See also R1073-R1081 and Q10955-6.																							
CC	Sequence 28 AA;																							

Query Match 100.0%; Score 202; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.00e-16;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 LVPNLGTREKRDSVCPOGKYIHPOXNSI 28
QY 1 lvpnlgtrekrdsvcpgkyihpqnsl 28
RESULT 2
ID R10984 standard; Protein; 102 AA.

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AC R10984;
DT 13-MAY-1991 (first entry)
DE Partial sequence 30kd TNF inhibitor.
KW Tumour necrosis factor; inhibitor.
OS Homo sapiens.
FH Key
FT region 1..52
FT region /label- exon I
FT region 53..95
FT region /label- exon II
FT region 96..102
FT region /label- exon III
FT region /note- "incomplete"
PN A09058976-A.
PD 24-JAN-1991.
PF 16-JUL-1990; 058976.
PR 18-JUL-1989; US-381080.
PR 11-DEC-1989; US-450329.
PR 07-FEB-1990; US-479661.
PA (SYNE-) STERGEN INC.
DR WPI; 91-073847/11.
DR N-PSDB; Q10878.
PT Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PS and -beta, useful as therapeutic agent.
PS Disclosure; Fig 13; 142pp; English.
CC The sequence comprises 48 residues of the 30 kd TNF inhibiting
CC glycoprotein, in three exons. The clone from which the sequence
CC was obd. was isolated from a human genomic library. The whole
CC gene can be inserted into expression vectors for prepn. of TNF
CC inhibitor for use in the treatment of inflammatory and degenerative
CC diseases.
CC See also R10986 and R11001.
SQ Sequence 102 AA;

Query Match 100.0%; Score 202; DB 1; Length 102;
Best Local Similarity 96.4%; Pred. No. 1.00e-16;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 17 LVPHLGDRERKDSVCPQGGKTIHPQNSI 44
1 LVPHLGDRERKDSVCPQGGKTIHPQNSI 28
QY 1 LVPHLGDRERKDSVCPQGGKTIHPQNSI 28

RESULT 3
ID R24082 standard; Protein; 154 AA.
AC R24082;
DT 05-NOV-1992 (first entry)
DE Truncated TNF-alpha 55kd receptor.
KW Tumour necrosis factor alpha; extracellular binding domain;
KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW malaria; viral meningitis; graft versus host disease;
KW autoimmune disease; rheumatoid arthritis.
OS Homo sapiens.
PD W09207076-A.
PD 30-APR-1992.
PF 18-OCT-1991; G01826.
PR 18-OCT-1990; GB-022648.
PA (CHAR-) CHARING CROSS SUNLEY RES CENT.
PA Brennan FM, Feldmann M, Gray PW, Turner MJC;
PI WPI; 92-167156/20.
DR N-PSDB; Q24443.
PT New polypeptide capable of binding human TNF alpha - comprises
PT first three cysteine-rich subdomains of TNF alpha receptor for
PT treating autoimmune disease, septic shock, HIV etc.
PS Example 1; Fig 9; 43pp; English.
CC This sequence is a truncated TNF-alpha receptor derivative
CC as encoded in pdeltairl. This was produced as described in
CC Q24443. This derivative lacks the third cysteine rich subdomain.
CC It could be used to regulate TNF-alpha mediated responses by binding
CC and sequestering human TNF-alpha e.g. in the treatment of pulmonary
CC diseases, septic shock, HIV infection, malaria, viral meningitis,
CC graft versus host disease and autoimmune diseases, esp. rheumatoid
CC diseases.
CC See also R24083.
SQ Sequence 102 AA;

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CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ Sequence 154 AA;

Query Match 100.0%; Score 202; DB 1; Length 154;
Best Local Similarity 96.4%; Pred. No. 1.00e-16;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 30 LVPHLGDRERKDSVCPQGGKTIHPQNSI 57
1 LVPHLGDRERKDSVCPQGGKTIHPQNSI 28
QY 1 LVPHLGDRERKDSVCPQGGKTIHPQNSI 28

RESULT 4
ID R24083 standard; Protein; 159 AA.
AC R24083;
DT 05-NOV-1992 (first entry)
DE Truncated TNF-alpha 55kd receptor.
KW Tumour necrosis factor alpha; extracellular binding domain;
KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW malaria; viral meningitis; graft versus host disease;
KW autoimmune disease; rheumatoid arthritis.
OS Homo sapiens.
PD W09207076-A.
PD 30-APR-1992.
PF 18-OCT-1991; G01826.
PR 18-OCT-1990; GB-022648.
PA (CHAR-) CHARING CROSS SUNLEY RES CENT.
PA Brennan FM, Feldmann M, Gray PW, Turner MJC;
PI WPI; 92-167156/20.
DR N-PSDB; Q24444.
PT New polypeptide capable of binding human TNF alpha - comprises
PT first three cysteine-rich subdomains of TNF alpha receptor for
PT treating autoimmune disease, septic shock, HIV etc.
PS Example 1; Fig 10; 43pp; English.
CC This sequence is a truncated TNF-alpha receptor derivative
CC as encoded in pdeltairl. This was produced as described in
CC Q24444. This derivative lacks the third cysteine rich subdomain.
CC It could be used to regulate TNF-alpha mediated responses by binding
CC and sequestering human TNF-alpha e.g. in the treatment of pulmonary
CC diseases, septic shock, HIV infection, malaria, viral meningitis,
CC graft versus host disease and autoimmune diseases, esp. rheumatoid
CC diseases.
CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ Sequence 159 AA;

Query Match 100.0%; Score 202; DB 1; Length 159;
Best Local Similarity 96.4%; Pred. No. 1.00e-16;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 30 LVPHLGDRERKDSVCPQGGKTIHPQNSI 57
1 LVPHLGDRERKDSVCPQGGKTIHPQNSI 28
QY 1 LVPHLGDRERKDSVCPQGGKTIHPQNSI 28

RESULT 5
ID R24084 standard; Protein; 168 AA.
AC R24084;
DT 05-NOV-1992 (first entry)
DE Truncated TNF-alpha 55kd receptor.
KW Tumour necrosis factor alpha; extracellular binding domain;
KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW malaria; viral meningitis; graft versus host disease;
KW autoimmune disease; rheumatoid arthritis.
OS Homo sapiens.
PD W09207076-A.
PD 30-APR-1992.
PF 18-OCT-1991; G01826.
PR 18-OCT-1990; GB-022648.
PA (CHAR-) CHARING CROSS SUNLEY RES CENT.
PA Brennan FM, Feldmann M, Gray PW, Turner MJC;
PI WPI; 92-167156/20.
DR N-PSDB; Q24445.
PT New polypeptide capable of binding human TNF alpha - comprises

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PT first three cysteine-rich subdomains of TNF alpha receptor for
 PS treating autoimmune disease, septic shock, HIV etc.
 CC Example 1; Fig 11; 43pp; English.
 CC This sequence is a truncated TNF-alpha receptor derivative, as
 CC encoded in pdeltar. This was produced as described in Q24445.
 CC This derivative lacks the membrane proximal 4th subdomain, yet
 CC retains the ability to bind TNF-alpha with high affinity
 CC (10power8 - 10power9 Mpower-1). The deriv. can be used in the
 CC regulation of TNF-alpha mediated responses by binding and
 CC sequestering human TNF-alpha e.g. in the treatment of pulmonary
 CC diseases, septic shock, HIV infection, malaria, viral meningitis,
 CC graft versus host disease and autoimmune diseases, esp. Rheumatoid
 CC arthritis. The deriv. is given at 10-100ug/dose.
 CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
 SQ Sequence 168 AA;

Query Match 100.0%; Score 202; DB 1; Length 168;
 Best Local Similarity 96.4%; Pred. No. 1.00e-16;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 30 LVPHLGDRERKDSVCPQKTYHPQNSI 57
 1 LVPHLGDRERKDSVCPQKTYHPQNSI 28

RESULT 6
 ID R24080 standard; Protein; 199 AA.
 AC R24080;
 DT 05-NOV-1992 (first entry)
 DE Truncated TNF-alpha 55kd receptor.
 KW Tumour necrosis factor alpha; extracellular binding domain;
 KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
 KW malaria; viral meningitis; graft versus host disease;
 KW autoimmune disease; rheumatoid arthritis.
 OS Homo sapiens.
 PN MO9207076-A.
 PD 30-APR-1992.
 PF 18-OCT-1991; GB-01826.
 PR 18-OCT-1990; GB-022648.
 PA (CHAR-) CHARING CROSS SUNLEY RES CENT.
 PI Brennan FM, Feldmann M, Gray FM, Turner MJC;
 DR WPI; 92-167156/20.
 DR N-PSDB; Q24441.

PT New polypeptide capable of binding human TNF alpha - comprises
 PT first three cysteine-rich subdomains of TNF alpha receptor for
 PT treating autoimmune disease, septic shock, HIV etc.
 PS Example; Fig 7; 43pp; English.
 CC This sequence is a truncated TNF-alpha receptor derivative, as encoded
 CC in pTNFrec. This was produced as described in Q24440.
 CC This derivative lacks the 81 carboxyl terminal residues of the
 CC cytoplasmic domain. The derivative could be used in the
 CC regulation of TNF-alpha mediated responses by binding and
 CC sequestering human TNF-alpha e.g. in the treatment of pulmonary
 CC diseases, septic shock, HIV infection, malaria, viral meningitis,
 CC graft versus host disease and autoimmune diseases, esp. Rheumatoid
 CC arthritis.
 CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
 SQ Sequence 199 AA;

Query Match 100.0%; Score 202; DB 1; Length 199;
 Best Local Similarity 96.4%; Pred. No. 1.00e-16;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 30 LVPHLGDRERKDSVCPQKTYHPQNSI 57
 1 LVPHLGDRERKDSVCPQKTYHPQNSI 28

RESULT 7
 ID W89225 standard; Protein; 211 AA.
 AC W89225;
 DT 04-MAR-1999 (first entry)
 DE Tumour necrosis factor Dp/osteoprotegerin construct TNFBp 4.0.

KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
 KW OP; chimeric; fusion; dimerisation domain; autoimmune disease;
 KW inflammation; apoptosis.
 OS Homo sapiens.
 OS Synthetic.
 PN MO9849305-A1.
 PD 05-NOV-1998;
 PF 29-APR-1998; U08631.
 PR 01-MAY-1997; US-850188.
 PA (AMGE-) AMGEN INC.
 PI Boyle WJ, Wooden S;
 DR WPI; 99-034661/03.
 PT New chimeric osteoprotegerin polypeptides - contain the
 PT osteoprotegerin dimerisation domain and a heterologous sequence,
 PT useful to treat TNF and TNFR-mediated disorders

PS Example 1; Fig 4; 92pp; English.
 CC The present invention describes a chimeric polypeptide (A1), comprising
 CC an osteoprotegerin (OP) dimerisation domain fused to a heterologous
 CC amino acid sequence. Also described are: (1) a multimer polypeptide
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid
 CC sequence; and (4) a host cell transformed or transfected with the
 CC expression vector so that the nucleic acid is expressible. The products
 CC from the present invention are useful to treat a variety of disorders
 CC including those related to receptor binding. Compositions comprising
 CC tumour necrosis factor (TNF)/OP and TNF receptor (TNFR)/OP chimeras
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
 CC autoimmune diseases and disorders related to excessive apoptosis. The
 CC chimeras are also useful for detecting molecules which interact with
 CC fused heterologous sequences to identify potential new receptors and
 CC ligands. The present sequence represents a TNFBp/OP construct from
 CC the example of the present invention for creating TNFBp/OP fusion
 CC proteins.
 SQ Sequence 211 AA;

Query Match 100.0%; Score 202; DB 1; Length 211;
 Best Local Similarity 96.4%; Pred. No. 1.00e-16;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 30 LVPHLGDRERKDSVCPQKTYHPQNSI 57
 1 LVPHLGDRERKDSVCPQKTYHPQNSI 28

RESULT 8
 ID R70108 standard; Protein; 309 AA.
 AC R70108;
 DT 10-NOV-1995 (first entry)
 DE TNF-R-GBPH fusion protein.
 KW Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
 KW red blood cell; cytokine receptor; glycoprotein binding peptide 130;
 KW GBP 130; GBPH; glycoprotein binding peptide homologue; glycoprotein A;
 KW tumour necrosis factor receptor; TNF-R.
 OS Chimeric Homo sapiens.
 OS Chimeric Plasmodium falciparum.
 PH Key Location/Qualifiers
 FT misc_difference 230..269
 FT /label="repeat_region
 FT /note="can be repeated n times, where n is a real
 FT number"

PD 09-MAR-1995.
 PF 01-SEP-1994; G01900.
 PR 03-SEP-1993; GB-018350.
 PR 23-AUG-1994; GB-017021.
 PA (PREN/) PRENDERGAST K F.
 PI Prendergast KF;
 DR WPI; 95-115452/15.
 PT New hybrid peptide(s) for binding cytokine(s) - comprising a
 PT malaria parasite peptide capable of binding a red blood cell and
 PT a receptor peptide.
 PS Example A; Page 54-55; 93pp; English.
 CC Hybrid peptides for binding cytokines, comprising a malaria parasite

CC (Plasmodium falciparum) peptide (capable of binding to a red blood cell (RBC)) and a receptor peptide are claimed. R70103-23 are examples of these hybrid peptides. R70108 is a fusion of tumour necrosis factor receptor (in accordance with R Loetscher et al Cell, Vol. 61, 351-359) and cyclophorin binding protein (GBP) homologue (GBPH). The use of cytokine receptors not normally found on RBCs means that the cytokine can bind harmlessly to the RBC without deleterious effect. CC The RBC protects the hybrid peptides from excretion from the kidney, and due to steric hindrance prevents the cytokines binding to a receptor in another cell. GBP 130 or GBPH are the pref. malaria parasite peptides used, others include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA (pre major merozoite surface antigen) and the Duffy binding receptor molecule (eg. exhibited by Plasmodium vivax). These peptides bind to pref. glycoprotein A, B and C, sialo glycoproteins, found on the surface of RBCs. The hybrid peptides are thus used to lower the levels of free CC cytokines in the circulation to reduce pathological damage.

SO Sequence 309 AA;

Query Match 100.0%; Score 202; DB 1; Length 309;
Best Local Similarity 96.4%; Pred. No. 1,00e-16;

Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 9 LYPHLDREKRDSCVPGKYIHPONNSI 36
OY 1 LYPHLDREKRDSCVPGKYIHPONNSI 28

RESULT 9
W89229 standard; Protein: 311 AA.

AC W89229; 04-MAR-1999 (first entry)
DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/304.
KW Tumour necrosis factor receptor 1; TNFR-1; Inhibitor; osteoprotegerin;
KM OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
OS Inflammation; apoptosis.
OS Homo sapiens.
ON Synthetic.
PN WO9849305-A1.
PD 05-NOV-1998.
PF 29-APR-1998; U08631.
PR 01-MAY-1997; US-850188.
PA (AMGE-) AMGEN INC.
PI Boyle WJ, Wooden S;
PT New chimeric osteoprotegerin polypeptides - contain the
PT osteoprotegerin dimerisation domain and a heterologous sequence,
PT useful to treat TNF and TNFR-mediated disorders
PS Example 1; Fig 4; 92pp; English.
CC The present invention describes a chimeric polypeptide (A1), comprising
CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
CC amino acid sequence. Also described are: (1) a multimer polypeptide
CC comprising covalently associated A1 monomers; (2) an isolated nucleic
CC acid encoding A1; (3) an expression vector comprising the nucleic acid
CC sequence; and (4) a host cell transformed or transfected with the
CC expression vector so that the nucleic acid is expressible. The products
CC from the present invention are useful to treat a variety of disorders
CC including those related to receptor binding. Compositions comprising
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
CC autoimmune diseases and disorders related to excessive apoptosis. The
CC chimeras are also useful for detecting molecules which interact with
CC fused heterologous sequences to identify potential new receptors and
CC ligands. The present sequence represents a TNFbp/OPG construct from
CC the example of the present invention for creating TNFbp/OPG fusion
CC proteins.
SO Sequence 311 AA;

Query Match 100.0%; Score 202; DB 1; Length 311;

Best Local Similarity 96.4%; Pred. No. 1,00e-16;

Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 30 LYPHLDREKRDSCVPGKYIHPONNSI 57

OY 1 LYPHLDREKRDSCVPGKYIHPONNSI 28

RESULT 10
W89228 standard; Protein: 366 AA.

ID W89228; 04-MAR-1999 (first entry)
DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/248.
KW Tumour necrosis factor receptor 1; TNFR-1; Inhibitor; osteoprotegerin;
KM OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
OS Inflammation; apoptosis.
OS Homo sapiens.
ON Synthetic.
PN WO9849305-A1.
PD 05-NOV-1998.
PF 29-APR-1998; U08631.
PR 01-MAY-1997; US-850188.
PA (AMGE-) AMGEN INC.
PI Boyle WJ, Wooden S;
PT New chimeric osteoprotegerin polypeptides - contain the
PT osteoprotegerin dimerisation domain and a heterologous sequence,
PT useful to treat TNF and TNFR-mediated disorders
PS Example 1; Fig 4; 92pp; English.
CC The present invention describes a chimeric polypeptide (A1), comprising
CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
CC amino acid sequence. Also described are: (1) a multimer polypeptide
CC comprising covalently associated A1 monomers; (2) an isolated nucleic
CC acid encoding A1; (3) an expression vector comprising the nucleic acid
CC sequence; and (4) a host cell transformed or transfected with the
CC expression vector so that the nucleic acid is expressible. The products
CC from the present invention are useful to treat a variety of disorders
CC including those related to receptor binding. Compositions comprising
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
CC autoimmune diseases and disorders related to excessive apoptosis. The
CC chimeras are also useful for detecting molecules which interact with
CC fused heterologous sequences to identify potential new receptors and
CC ligands. The present sequence represents a TNFbp/OPG construct from
CC the example of the present invention for creating TNFbp/OPG fusion
CC proteins.
SO Sequence 366 AA;

Query Match 100.0%; Score 202; DB 1; Length 366;
Best Local Similarity 96.4%; Pred. No. 1,00e-16;

Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 30 LYPHLDREKRDSCVPGKYIHPONNSI 57
OY 1 LYPHLDREKRDSCVPGKYIHPONNSI 28

RESULT 11
R07449 standard; Protein: 371 AA.
ID R07449; 29-JUN-1991 (first entry)
DE Tumour Necrosis Factor-Binding Protein from PTFN-BP15 CDNA.
KW Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KM TNF-BP15; infectious disease; parasitic disease; cachexia;
KW autoimmune disease; shock.
OS Homo sapiens.
ON EP-393438-A.
PN 24-OCT-1990.
PF 06-APR-1990; 106624.
PR 21-APR-1989; DE-913101.
PR 21-JUN-1989; DE-920282.
PA (BOEH) BOEHRINGER INGELHEIMINT.
PI Hauptmann R, Himmeler A, Maurer-Fogy I, Stratowa C;
DR N-PSDB; Q06282.
PT DNA encoding TNF binding protein and TNF-receptor - used in
PT tumour treatment and to understand mechanism to TNF action
PT disclosure; Fig 1(1-3); 51pp; German.

CC Clone pTNF-BP15 was used to construct pADTNF-BP, for transfection of
 CC e.g. COS7 cells. The expressed proteins are useful
 CC prophylactically and therapeutically to control disorders which
 CC involve the damaging effects of TNF: alpha or beta (e.g. infectious or
 CC parasitic diseases, shock, cachexia, autoimmune diseases, adult
 CC respiratory distress syndrome etc.), or side effects of treatment with
 CC TNF-alpha). They can also be used as diagnostic reagents for
 CC assaying TNF and in study of TNF-receptor interactions.
 CC See also 006282-006285.
 SQ Sequence 371 AA;

Query Match 100.0%; Score 202; DB 1; Length 371;
 Best Local Similarity 96.4%; Pred. No. 1.00e-16;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 30 LVPHLDREKRDVCPQKGYHPQNNST 57
 OY 1 LVPHLDREKRDVCPQKGYHPQNNST 28

RESULT 12
 ID W89227 standard; Protein; 397 AA.
 AC W89227;
 DT 04-MAR-1999 (first entry)
 DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/217.
 KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
 KW Inflammation; apoptosis.
 OS Homo sapiens.
 OS Synthetic.
 PN MO9849305-A1.
 PD 05-NOV-1998.
 PF 29-APR-1998; U08631.
 PR 01-MAY-1997; US-850188.
 PA (AMGE-) AMGEN INC.
 PI Boyle WJ, Wooden S;
 PT WPI; 99-034661/03.
 PT New chimeric osteoprotegerin polypeptides - contain the
 PT osteoprotegerin dimerisation domain and a heterologous sequence,
 PT useful to treat TNF and TNFR-mediated disorders

PS Example 1; Fig 4; 92pp; English.
 CC The present invention describes a chimeric polypeptide (A1), comprising
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
 CC amino acid sequence. Also described are: (1) a multimer polypeptide
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid
 CC sequence; and (4) a host cell transformed or transfected with the
 CC expression vector so that the nucleic acid is expressible. The products
 CC from the present invention are useful to treat a variety of disorders
 CC including those related to receptor binding. Compositions comprising
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
 CC autoimmune diseases and disorders related to excessive apoptosis. The
 CC chimeras are also useful for detecting molecules which interact with
 CC fused heterologous sequences to identify potential new receptors and
 CC ligands. The present sequence represents a TNFbp/OPG construct from
 CC the example of the present invention for creating TNFbp/OPG fusion
 CC proteins.
 SQ Sequence 397 AA;

Query Match 100.0%; Score 202; DB 1; Length 397;
 Best Local Similarity 96.4%; Pred. No. 1.00e-16;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 30 LVPHLDREKRDVCPQKGYHPQNNST 57
 OY 1 LVPHLDREKRDVCPQKGYHPQNNST 28

RESULT 13
 ID W89226 standard; Protein; 417 AA.
 AC W89226;
 DT 04-MAR-1999 (first entry)

DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/196.
 KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
 KW Inflammation; apoptosis.
 OS Homo sapiens.
 OS Synthetic.
 PN MO9849305-A1.
 PD 05-NOV-1998.
 PF 29-APR-1998; U08631.
 PR 01-MAY-1997; US-850188.
 PA (AMGE-) AMGEN INC.
 PI Boyle WJ, Wooden S;
 PT WPI; 99-034661/03.
 PT New chimeric osteoprotegerin polypeptides - contain the
 PT osteoprotegerin dimerisation domain and a heterologous sequence,
 PT useful to treat TNF and TNFR-mediated disorders

PS Example 1; Fig 4; 92pp; English.
 CC The present invention describes a chimeric polypeptide (A1), comprising
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
 CC amino acid sequence. Also described are: (1) a multimer polypeptide
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid
 CC sequence; and (4) a host cell transformed or transfected with the
 CC expression vector so that the nucleic acid is expressible. The products
 CC from the present invention are useful to treat a variety of disorders
 CC including those related to receptor binding. Compositions comprising
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
 CC autoimmune diseases and disorders related to excessive apoptosis. The
 CC chimeras are also useful for detecting molecules which interact with
 CC fused heterologous sequences to identify potential new receptors and
 CC ligands. The present sequence represents a TNFbp/OPG construct from
 CC the example of the present invention for creating TNFbp/OPG fusion
 CC proteins.
 SQ Sequence 417 AA;

Query Match 100.0%; Score 202; DB 1; Length 417;
 Best Local Similarity 96.4%; Pred. No. 1.00e-16;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 30 LVPHLDREKRDVCPQKGYHPQNNST 57
 OY 1 LVPHLDREKRDVCPQKGYHPQNNST 28

RESULT 14
 ID W89224 standard; Protein; 420 AA.
 AC W89224;
 DT 04-MAR-1999 (first entry)
 DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/OPG.
 KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
 KW Inflammation; apoptosis.
 OS Homo sapiens.
 OS Synthetic.
 PN MO9849305-A1.
 PD 05-NOV-1998.
 PF 29-APR-1998; U08631.
 PR 01-MAY-1997; US-850188.
 PA (AMGE-) AMGEN INC.
 PI Boyle WJ, Wooden S;
 PT WPI; 99-034661/03.
 PT New chimeric osteoprotegerin polypeptides - contain the
 PT osteoprotegerin dimerisation domain and a heterologous sequence,
 PT useful to treat TNF and TNFR-mediated disorders

PS Example 1; Fig 4; 92pp; English.
 CC The present invention describes a chimeric polypeptide (A1), comprising
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
 CC amino acid sequence. Also described are: (1) a multimer polypeptide
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid
 CC sequence; and (4) a host cell transformed or transfected with the
 CC expression vector so that the nucleic acid is expressible. The products

from the present invention are useful to treat a variety of disorders
 including those related to receptor binding. Compositions comprising
 tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
 are used to treat TNF and TNFR-mediated disorders such as inflammation,
 autoimmune diseases and disorders related to excessive apoptosis. The
 chimeras are also useful for detecting molecules which interact with
 fused heterologous sequences to identify potential new receptors and
 ligands. The present sequence represents a TNFbp/OPG construct from
 the example of the present invention for creating TNFbp/OPG fusion
 proteins.

CC from the present invention are useful to treat a variety of disorders
 CC including those related to receptor binding. Compositions comprising
 CC tumor necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
 CC autoimmune diseases and disorders related to excessive apoptosis. The
 CC chimeras are also useful for detecting molecules which interact with
 CC fused heterologous sequences to identify potential new receptors and
 CC ligands. The present sequence represents a TNFp/OPG construct from
 CC the example of the present invention for creating TNFp/OPG fusion
 CC proteins.
 SQ Sequence 420 AA;

Query Match 100.0%; Score 202; DB 1; Length 420;

Best Local Similarity 96.4%; Pred. No. 1.00e-16;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 30 LVPHLGDERKRDVCPQGIHPONNSI 57
 1 lvpplgdrkrdsvcpqgkylhpqxnsl 28

RESULT 15
 ID R51032 standard; Protein; 433 AA.
 AC R51032;
 DT 13-MAY-1994 (first entry)
 DE Mutant p55 tumour necrosis factor receptor.
 KW TNF; tumour necrosis factor; receptor; disease; autoimmunity;
 KW rheumatoid arthritis; graft rejection; graft vs. host; septic shock;
 KW effector protein.
 OS Homo sapiens.
 FH Key location/Qualifiers
 FT region 1..21
 FT domain /label= leader peptide.
 FT 183..205 /label= transmembrane domain.
 PN EP-568925-A.
 PD 10-NOV-1993.
 PE 29-APR-1993; 106981.
 PR 03-MAY-1992; IL-101769.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PI Brakelbusch C, Wallach D;
 DR N-PSDB: 050870.
 PT Modulating activity of tumour necrosis factor receptor - using
 PT peptide(s), antibodies, etc. which interact with critical regions
 PT of receptor or effector protein, for controlling auto-immune
 PT disease, septic shock, etc.
 PS Claim 4; Figure 1; 17pp; English.
 CC Modification of the tumour necrosis factor receptor by mutation or
 CC deletion modulates signal transduction and/or cleavage effected by
 CC the receptor. This modulation of activity can also be achieved
 CC using effector proteins which interact with the TNF receptor.
 CC Molecules which interact with the TNF receptor or the effector
 CC proteins can be used to treat or prevent diseases associated with
 CC TNF activity e.g. autoimmune disease; rheumatoid arthritis; graft
 CC rejection; graft vs. host disease or septic shock. They can also
 CC be used to treat overdoses of exogenous TNF. Specific deletions
 CC include amino acid residues 405-426 (to give this sequence, wild
 CC type protein disclosed in R42197) from which it was discovered
 CC that amino acids 405-414, or part of them, are essential for the
 CC signalling of the human p55 TNF-R for the cytotoxic effect of TNF
 CC whereas amino acids 415-426 are not essential. Also residues
 CC 170-174, 174-179 or both 170-179 were deleted. This region of
 CC amino acids, or part of, when deleted, abolished shedding of the
 CC soluble extracellular forms of the protein.
 SQ Sequence 433 AA;

Query Match 100.0%; Score 202; DB 1; Length 433;

Best Local Similarity 96.4%; Pred. No. 1.00e-16;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 30 LVPHLGDERKRDVCPQGIHPONNSI 57
 1 lvpplgdrkrdsvcpqgkylhpqxnsl 28

QY 1 lvpplgdrkrdsvcpqgkylhpqxnsl 28
 Search completed: Tue Apr 18 11:05:38 2000
 Job time : 28 secs.